SEARCH REQUEST FORM

7.511

Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s). Please Search SEQ ID 100:1-3 Please Do an interfere sequence search of the sequences, please attach a copy of the sequences. You may include a copy of the broadest and/or most relevant claim(s). Please Do an interfere sequences, please attach a copy of the broadest and/or most relevant claim(s). Please Do 10:1-3. Please Do 10:1-3.		Requestor's Name: Name Name Serial Number: 09/047,652 Date: 7-2098 Phone: 305-5860 Art Unit: 1642
Plass do an interference search of Soy Ib No:1-3. Peturn on Paper print out. Thomas! Wany).		Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach
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MPsrch_nn n.a n.a. database search, using Smith-W	Smith-Waterman algorithm
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Title: >US-09-047-652A-1 Description: (1-652) from US09047652A.seq Perfect Score: 652 N.A. Sequence: 1 CCACGGCGAAGGTCTCCGCT	GITCITGGAACAIGGAAIIT 652 .CAAGAACCIIGTACCIIAAA
Scoring table: TABLE default Gap 6	
Nmatch STD : Dbase 0; Query 0	
Searched: 457396 segs, 834342348 bases x 2	
Post-processing: Minimum Match 0% Listing first 45 summaries	
Database: embl54 1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:e genbank106 13:9b_ba 14:9b_htg 15:9b_in 16:9b_om 19:9b_ph 20:9b_pl 21:9b_pr1 22:9b_pr2 25:9b_sy 26:9b_un 27:9b_pr1 22:9b_pr2	m2 5:em_in 6:em_om 11:em_ro 12:em_vi om 17:gb_ov 18:gb_pat pr2 23:gb_ro 24:gb_st
Statistics: Mean 10.377; Variance 5.497; scale 1	1.888
Pred. No. is the number of results predicted by c score greater than or equal to the score of the r and is derived by analysis of the total score dis	chance to have a result being printed, istribution.
SUMMARIES	
Result Query No. Score Match Length DB ID Description	on Pred. No.
643 98.6 821 21 HUMHPBS Humar 542 83.1 639 21 HUMBENZA Humar 403 61.8 684 21 HSPBR4 Humar 403 61.8 160559 14 HSI191B2 Humar 402 61.7 4258 21 HSJ12421 Humar 384 58.9 152843 14 HS526114 Humar 288 44.2 821 16 BOVPBRIBP Calf	0000000
3 626 3 MUSMPBR 3 781 23 RATPKBSX 0 856 23 MUSPTBR 6 645 21 HSPBR3 6 343 42 RATPTBZR02 3 487 21 HSPBR2 0 7218 18 166494 7 1084 23 CGU12420	-type 8 Ype be 4 eriphe 1 benzo 6 Ype be 3 Ype be 3 Penzo 2 paten 1

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Sequence of Low Mus musculus mit Sequence 5 from Carotenoid gene R.sphaeroides cr	Homo sapiens calcium-a Homo sapiens calcium-a Homo sapiens intermedi A.hydrophila amonabact Human tristetraproline H.sapiens zinc finger	Homo sapiens intermedi Homo sapiens intermedi Homo sapiens zinc fing Mycobacterium smegmati Mycobacterium smegmati Homo sapiens WSCR4 qen	ntrB, ntrC [Azosp Homo sapiens mRNA Rattus norvegicus Mouse opsin (MOPS	Homo Sapiens PAC Clone Sequence 142 from pate Human placental alkali	Human alkaline phospha Human placental alkali Cloning vector pSEAP2-	Rhodobacter cap Homo sapiens ch *** SEQUENCING	ENTS PRI PRI POLITY PRI PRI PRI PRI PRI PRI PRI PRI PRI PR
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1525 215 3084 9298	1284 1284 1328 1684 1746	1982 2238 3889 196 1120	2926 4943 5350 9483	134914	2688 5115	10068 119307 276261	HUMHPBS 821 bp mF Human peripheral benzodlaz M36035 9184333 peripheral benzodlazepine Human cDNA to mRNA. Homo sapiens Eukaryotae: mitochondrial Vertebrata: Eutheria: Prim 1 (bases 1 to 821); Kag Kiond, J., Mattel, M.G., Kag Fur, G., Caput, D. and Ferra Molecular cloning and chro peripheral type benzodlaze Eur. J. Blochem. 195 (2), 9114656 2 (bases 1 to 821) Riond, J. Direct Submission Submitted (27-JUN-1990) J. 31328 Labege Cedex, France Location/Qualifie 1. 821 //organism="homo s/db_rref="peripheral //ordal-peripheral //ordal-peripheral //odb_rref="peripheral //odb_rref="peripheral //codon_start=1 //db_rref="peripheral //codon_start=1 //db_rref="peripheral //codon_start=1 //db_rref="peripheral //codon_start=1 //db_rref="peripheral
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 684) Lin.D.; Chang, Y.J.; Strauss, J.F. and Miller, W.L. The human peripheral benzodiazepine receptor gene: cloning and
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/product="peripheral benzodiazepine receptor related
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                /tissue_type="placenta"
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    /db_xref="taxon:9606"
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Lin, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.
The humn peripheral benzodiazepine receptor gene: cloning characterization of alternative splicing in normal tissues gentient with congenital lipoid adrenal hyperplasia genomics 18 (3), 643-650 (1993)
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                                                          Length 821,
                                                        Score 643; DB 21; Length 82
Pred. No. 0.00e+00;
0; Mismatches 5; Indels
                   others
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118 a 271 c 260 g 171
Chromosome 22, map position q13.3.
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llarity 99.2%;
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POLYA_signal
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DEFINITION

ACCESSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

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JOURNAL MEDLINE FEATURES

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characterization of alternative splicing in normal tissues and in
patient with congenital lipoid adrenal hyperplasia
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Submitted (23-MAR-1998) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CBIO 15A, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
1191B2; HTGS phase 1.
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Primates; Catarrhin; Hominidae; Homo.
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/db_xref="taxon:9606"
/tissue_type="placenta"
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/tissue_lib="placenta"
join(Li1952:195 .376,L21953:224 .362,164 .352)
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/product="peripheral benzodiazepine receptor"
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ARPONING THIS Sequence 1s unitained and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be econtaminated with foreign sequence. Ecoli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate sequence. By continuins a sequence: bkill9182 Contig_ID: 01507 acc_ Length: 2099 bp Unfinished sequence: bkill9182 Contig_ID: 01607 acc_ Length: 5280 bp Unfinished sequence: bkill9182 Contig_ID: 01201 acc_ Length: 1183 bp Unfinished sequence: bkill9182 Contig_ID: 01500 acc_ Length: 1183 bp Unfinished sequence: bkill9182 Contig_ID: 00949 acc_ Length: 6912 bp Unfinished sequence: bkill9182 Contig_ID: 00949 acc_ Length: 6912 bp Unfinished sequence: bkill9182 Contig_ID: 00949 acc_ Length: 6912 bp Unfinished sequence: bkill9182 Contig_ID: 00949 acc_ Length: 6912 bp Unfinished sequence: bkill9182 Contig_ID: 00949 acc_ Length: 6912 bp Unfinished sequence: bkill9182 Contig_ID: 00946 acc_ Length: 2136 bp Unfinished sequence: bkill9182 Contig_ID: 00946 acc_ Length: 2136 bp Unfinished sequence: bkill9182 Contig_ID: 01825 acc_ Length: 5412 bp Unfinished sequence: bkill9182 Contig_ID: 01823 acc_ Length: 542 bp Unfinished sequence: bkill9182 Contig_ID: 01831 acc_ Length: 542 bp Unfinished sequence: bkill9182 Contig_ID: 01825 acc_ Length: 12009 bp Unfinished sequence: bkill9182 Contig_ID: 01829 acc_ Length: 12009 bp Unfinished sequence: bkill9182 Contig_ID: 01825 acc_ Length: 12009 bp Unfinished sequence: bkill9182 Contig_ID: 01825 acc_ Length: 12009 bp Unfinished sequence: bkill9182 Contig_ID: 01832 acc_ Length: 1799 buffinished sequence: bkill9182 Contig_ID: 01832 acc_ Length: 1799 buffinished sequence: bkill9182 Contig_ID: 00050 acc_ Length: 1751 bp Unfinished sequence: bkill9182 Contig_ID: 00050 acc_ Length: 1751 bp Unfinished sequence: bkill9182 Contig_ID: 00050 acc_ Length: 1751 bp Unfinished sequence: bkill9182 Contig_ID: 00050 acc_ Length: 1751 bp Un
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IMPORTANT: This sequence is unfinished and does not necessarily
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* the sequence data presented in this record will be replaced

*by a single finished sequence with the same accession number

Location/Qualifiers
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Pred. No. 3.85e-288;
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/db_xref="taxon:9606"
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Krueger, K.E.
Direct Submission
Submitted (19-JU-1994) Karl E. Krueger, Dept. of Cell Biology,
Georgetown University School of Medicine, Washington, DC 20007, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="mitochondrial benzodiazepine receptor"
/db_xref="PID:9529946"
/db_xref="PID:9529946"
/translation="MarpwrPamGFTLAPSLGCFVGSRFVHGEGLRWYAGLQKPSWHP
PHWVLGPVWGTLYSAMAGYGSYLVWKELGGFFEKAVVPLGLYTGGLALWWAWPFIFFGA
RQMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAFTTLUYCVWRDNHG
                                                                                                                                                                                                                                                                                                                             human and
HSU12421 4258 bp DNA PRI 14-DEC-1995
Human mitochondrial benzodiazepine receptor (MBR) gene, complete
                                                                                                                                                                                                                                                                       1 (bases 2080 to 3683)
Yakovlev, A.G., Ruffo,M., Jurka,J. and Krueger,K.E.
Comparison of repetitive elements in the third intron of hun
rodent mitochondrial benzodiazepine receptor-encoding genes
Gene 155 (2), 201-205 (1995)
                                                                                                                                                                                                                                                       Nomo sapiens
Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarihini; Hominidae; Homo.
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/product="mitochondrial benzodiazepine receptor"
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/product="mitochondrial benzodiazepine receptor"
                                                            71600 GGTAGTGGCTGCCGCCCCCCACTGACCAGCAGGAGTCCACCAAGGCC 71648
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/gene="MBR"
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/db_xref-"taxon:9606"
/map-"22q13.3"
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/note="4 Alus"
/rpt_family="Alu"
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represent the correct sequence. Work on the sequence is in progress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 18A, UK. B-mail enquires: humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk IMPORTANT: This sequence is unfinished and does not necessarily
                                                                                                                                                                                                                                                                                                                             3683 GGCCTTGGTGGATCTCCTGCTGGTCAGTGGGGCGGCGGCGCCACCTACCGTGCCTGGTA 3742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363
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                                                                                                                                                                                                                                                                                                                                                        HS526I14 152843 bp DNA HTG 13-JAN-1997
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
526I14; HTGS phase 1.
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152843)
Buck,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 TGTGATGTGGTGGCCGTCACGCTTTCATGACCACTGGGCCTGCTAGTCTGTCAGGGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
/product="mitochondrial benzodiazepine receptor"
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Pred. No. 2.43e-287;
0; Mismatches 0;
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/rpt_family="MIR"
3684. .4122
/number=4
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99.8%;
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Pred. No. 5.93e-273;
0; Mismatches 5; Indels 3;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="526114"
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Best Local Similarity 98.1%;
Matches 404; Conservative
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/db_xref-"PID:g163489"
/translat.ton="MAPPWPAVGFTLLPSLGGFLGAQYTRGEGFRWYASLQKPPWHP
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RQMGWALVDLLLTGGWAAATAWAWHQVSPPAACLLYPYLAWLAFAGMLNYRMWQDNQV
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Verkaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
I (Dases I to 821)
Parola,A.L., Stump,D.G., Pepper,D.J., Krueger,K.E., Regan,J.W. and
                                                                                                                                                receptor isoquinoline binding
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/product="benzodiazepine receptor isoquinoline binding
protein"
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9163488
benzodlazepine receptor isoquinoline binding protein.
Calf adrenal gland, cDNA to mRNA.
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Pred. No. 1.44e-196;
0; Mismatches 81;
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Russell"
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J. Biol. Chem. 266, 14082-14087 (1991)
91310699
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Calf peripheral-type benzodiazepine r
protein (PBR/IBP) mRNA, complete cds.
M64520
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/db_xref="taxon:9913"
/dev_stage="calf"
/tissue_type="adrenal gl
/tissue_lib="of David Ru
67. .806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .821
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/gene="PBR/IBP"
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Local Similarity 82.1%;
les 381; Conservative
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ROMGWALADLLLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATVLNYYWRDNSG
RRGGSRLPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="peripheral-type benzodiazepine receptor"
/db_xref="PID:g309442"
/translation="MPESWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                                                  MUSAMPBR 626 bp mRNA ROD 27-JUL-1994
MOUSE peripheral-type benzodlazepine receptor mRNA, complete cds.
L17306
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 626)
Garnier, M., Dimchev, A.B., Boujrad, N., Price, J.M., Musto, N.A. and
Papadopoulos, V.
                                                      563
                                                                   GCCTTGGCCGATCTTCTGCTTGTCAGTGGGGTGGCGACTGCCACAACCCTGGCTTGGCAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAAAGAGCTGGGAGGTTTCACAGAGGACGCTATGGTTCCCTTGGGTCTCTACACTGGT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 GGCGAGGGCCTCCGGTGGTATGCTAGCTTGCAGAACCCTCTTGGCATCCGCCTCGCTGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ACACTGGCTCCCATCTGGGGCACACTGTATTCAGCCATGGGGTATGGCTCCTACATAGTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGAAGGTCTCCGCTGCTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
GCACCAGGTGAGCCCGCCGGCTGCCTGCTGTACCCGTACCTGGCCTGGCTGCCTT
                         301 GTACCAGGTGAGCCCGCTGGCCGCCCGCTGTTACCCCTACCTGGCCTGGCCTT
                                                     504 TGCCGGCATGCTCAACTACCGCATGTGGCAGGACAACCAGGTCCGGAGGAGTGGCCGGCG
                                                                                                                                                                                                                                                                                                                                                         In vitro reconstitution of a functional peripheral-type benzodizepine receptor from mouse Leydig tumor cells Mol. Pharmacol. 45 (2), 201-211 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 282; DB 23; Length 626
Pred. No. 8.06e-192;
0; Mismatches 91; Indels
                                                                                                         9309411
benzodlazepine receptor.
Mus musculus mouse testis tumor cDNA to mRNA
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mouse testis tumor" 31. .540 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="MA-10"
/cell_type="leydig"
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Best Local Similarity 80.4%;
Matches 373; Conservative
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                                                                                                                                                                                                                                                                                                                     Murinae; Mus.
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Murinae; Rattus.
Murinae; Rattus.

(Jases I to 781)
Sprengel,R., Werner,P., Seeburg,P.H., Mukhin,A.G., Santi,M.R.,
Grayson,D.R., Guidotti,A. and Krueger,R.E.
Molecular cloning and expression of cDNA encoding a peripheral-type bensodiazepine receptor
J. Biol. Chem. 264, 20415-20421 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xxef="PID:g206162"
/translation="MSQSWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
PRWTLAPIWGTLYSAMGYGSYTIWKELGGFPERAMVPLGLYTGQLALWWAWPIFFGA
RQMGWALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATMLNYYWRDNSG
RRGGSRITT"
765. .770
                                                                                                                                                                                                                                                                                        RATPKBSX 781 bp mRNA ROD 12-JUN-1992
Rat peripheral-type benzodlazepine receptor (PKBS) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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412 CGAGTGAGCCCGCCGGCTGCCGCTTGCTGTACCCTTACCTGGCCTGGCTTGTTTGCC 471
                                                                                                    116 GGTGAGGGCCTCCGCTGGTATGCTAGCTTGCAGAAACCCTCCTGGCATCCGCCTCGCTGG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Draft entry and computer readable copy of sequence [1] kindly provided by Krueger, K.E., 20-SEP-1989.
Localion/Qualifiers
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                       GCTTTGGTGGACCTCATGCTTGTCAGTGGGGTGGCAACCGCCACTACCCTGGCTTGGCAC
                                                                               472 ACCGIGCICAACIACIAIGIAIGICGCGCGAIAACICIGGCCGGCGGGGGGCTCCCGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="peripheral-type benzodlazepine receptor"
/codon_start=1
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Pred. No. 4.49e-187;
0; Mismatches 77; Indels
                                                                                                                                                              532 CCAGAGTGAAGGCACCCAGCCATCAGGAATGCAGCCTGCCAGC 575
                                                                                                                                                                                      peripheral-type benzodiazepine receptor.
Rat adult adrenal cortex, cDNA to mRNA.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 781. /organism="Rattus norvegicus" /db_xref="taxon:10116" 35. .544
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ilarity 82.1%;
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Best Local Similarity
Matches 353; Conser
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Submitted (15-OCT-1993) to the DDBJ/EMBL/GenBank databases. Shigeru
Taketani, Kansai Medical University, Dept. of Hygiene; 10-15
Fumizono-cho, Moriguchi, Osaka 570, Japan
(Tel:06-992-1001(ex.2004), Fax:06-992-3522)
Submitted (15-Oct-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"peripheral-type benzodiazepine receptor"
/db_xref-"PID:d1005281"
/db_xref-"PID:q484054"
/db_xref-"PID:q884054"
/translation-"MPEXMAVGLILVPSLGGFMGAYFVRGEGLRWYASLOKPSWHP
PRWTLAPIWATLYSAMGYGSYIVWKELGGFFEDAMVPLGLYGGLALWWANPPIFFGA
RQMGWALADLLLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATVLNYYWRDNSG
                                                                                                                                                                                                                                                                               peripheral-type benzodiazepine receptor.
Mus musculus cell-line erythroleukemia (library: lambda gtll) cDNA
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                                                                                                                                                                                                                             Mouse mRNA for peripheral type benzodiazepine receptor, complete
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Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                    364
                                                                             476 ACCATGCTCAACTACTATGTATGCGTGATAACTCTGGTCGGCGGGGGGGCTCCCGGCTC 535
245 GCCTTGGTGGATCTCCTGCTGGTCAGTGGGGGGGGGGGCAGCCACTACCGTGGCCTGGTAC 304
                                                                                         27-MAR-1996
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                                         416 CGAGTGAGCCCACCGGCTGCCCGCTTGCTGTATCCTTACCTGGCCTGGCTTTGCC
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Pred. No. 1.71e-185;
0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="erythroleukemia"
/clone_lib="lambda gtil"
66. .575
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Kansai Medical University
1-Fumizonocho, Moriguchi
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06-992-3522.
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Best Local Similarity 79.5%;
Matches 369; Conservative
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254 c
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Phone:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 ACCGTGCTCAACTACTATGTATGGCGTGATAACTCTGGCCGGCGAGGGGGCTCCCGGCTC 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 CCCCTGGGCCTCTACACTGGGCAGCTGGCCTGAACTGGGCATGGCCCCCCATCTTCTT 341
                                                                            267 IGGAAAGAGCIGGGAGGIITCACAGAGGACGCIAIGGIICCCIIGGGICICIACACIGGI 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ызгыкы 645 bp DNA PRI 20-MAY-1994
Human peripheral benzodlazepine receptor gene, exon 3.
L21953
64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    benzodiazepine receptor; peripheral benzodiazepine receptor
                                                                                                                                                                                                                                                   327 CAGCTGGCTCTGAACTGGGCGTGGCCCCCCATCTTTTGTTGGTGCCCGGCAGATGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GGCGAAGGTCTCCGCTGGTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGG
                                               207 ACACTGGCTCCCATCTGGGCAACACTGTATTCAGCCATGGGGTATGGCTCCTACATAGTC
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177 c 192 g 138 t
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Pred. No. 6.34e-72;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 GCAGAGTGAAGGCACCCAGCCATCAGGAATGCAGCCCTGCCAGC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 CCAGAGTGAGTGCCCGGCCCAGGGACTGCAGCTGCACCAGC 468
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/organism="Homo sapiens"
/db.xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
224. 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .645
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Best Local Similarity 98.6%;
Matches 140; Conservative
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DEFINITION

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KEYWORDS SEGMENT SOURCE

ORGANISM

REFERENCE AUTHORS MEDLINE REFERENCE

JOURNAL

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AUTHORS

MEDLINE COMMENT

FEATURES

JOURNAL

TITLE

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1986 CCTTGGGTCTCTACACTGGTCAGCTGGCTCTGAACTGGGCCATGCCCCCCATCTTTG 2045
     105 GGTACGGCTCCTACCTGGAAAGAGCTGGGAGGCTTCACAGAGAAGGCTGTGGTTC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 CCACGGCGAGGGTCTCCGCTGGTACGCCGGCCTGCAGAGCCCTCGTGGCACCCGCCCCA 331
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Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.
The human peripheral benzodiazepine receptor gene: cloning an characterization of alternative splicing in normal tissues apatient with congenital lipoid adrenal hyperplasia galludista 18, 643-650 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    benzodiazepine receptor; peripheral benzodiazepine receptor. 2 of 4 Homo sapiens DNA. Homo sapiens
                                                                                           1...487
/organism="Homo sapiens"
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/tissue_ltype="placenta"
/tissue_ltb="placenta"
166..376
/product="peripheral benzodiazepine receptor"
/fisheral for the force of the force 
                                                                                                                                                                                                                                                                                                 пэгыка
Human peripheral benzodiazepine receptor gene, exon 2.
g483403
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Pred. No. 2.10e-55;
0; Mismatches 1; Indels
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Unclassified.
1 (bases 1 to 7218)
Dorner,F., Scheifilinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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Sequence 14 from patent US 5670367.
166494
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1491 c 1486 g
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Best Local Similarity 99.1%;
Matches 107; Conservative
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SOURCE
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ACCESSION
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ORIGIN
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TITLE
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FEATURES
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Molecular Cloning and Expression of CDNA Encoding a Peripheral-type
Benzodiazepine Receptor
J. Baol. Chem. 264, 20415-20421 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/product="peripheral-type benzodiazepine receptor"
/blaxref="piD:9206480"
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PRWTLAPIWGTLYSAMGYGSYIIWKELGGFFEEAMVPLGLYTGQLALWWANPPIFFGA
RQMGWALVDLALVSGVATATLAWHRVSPPAARLLYPYLAWLAFATMLNYYWRDNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure of the rat gene encoding the mitochondrial benzodiazepine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 3434)
Casalotti.5.O., Pelala,G., Yakovlev,A.G., Csikos,T., Grayson,D.R.
and Krueger,K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence M84221 starts with a Bam HI site, leaving a gap of about 7kb between sequences. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Butheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

(bases 1 to 3434)
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164 CCCCTGGGCCTCTACACTGGGCAGCTGGCCCTGAACTGGGCATGGCCCCCCATCTTT 223
                                                                                                                                                                                                                               25-JAN-1993
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                                                                                                                                                                                                RATPTBZRO2 3434 bp DNA ROD 25-JAN-19
Rat peripheral-type benzodiazepine receptor gene exons 2-4,
complete cds.
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Pred. No. 3.97e-62;
0; Mismatches 13; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                     2 of 2
Rattus norvegicus (strain Wistar) Adult DNA.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
order(M95864:1273. .1462,1. .1094)
                                                                                                                                                                                                                                                                                                                                                              peripheral-type benzodiazepine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .3434
/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
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/note="putative"
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                                                   342 GGTGCCCGACAATGGGCTGGG 363
                                                                                   224 GGTGCCCGACAAATGGGCTGGG 245
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/number=3
2066. .2924
/number=3
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/number=4
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Best Local Similarity 90.8%;
Matches 128; Conservative
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Submitted (19-JUL-1994) Karl E. Krueger, Dept. of Cell Biology,
Georgetown University School of Medicine, Washington, DC 20007, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chinese hamster.
Cricetulus griseus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Cricetinae; Cricetulus.
1 (bases 41 to 1029)
Yakovlev,A.G., Ruffo,M., Jurka,J. and Krueger,K.E.
Comparison of repetitive elements in the third intron of human and rodent mitochondrial benzodiazepine receptor-encoding genes
Gene 155 (2), 201-205 (1995)
                 ö
                                               193 CCTGAACTGGGCATGCCCCCATCTTTGGTGCCCGACAAATGGGCTGGGCCTTGGT 252
                                                                                                                                     133 GCTGGGAGGCTTCACAGAGAAGGCTGTGGGTTCCCCTGGGCCTCTACACTGGGCAGCTGGC 192
                                                                                                                                                                                                                                                                                                                                     253 GGATCTCCTGCTGGTCAGTGGGGGGGGGGGCACCACTACCGTGGCCTGGTACCAGGTGAG 312
                                                                                                                                                                                                                                                                                                                                                                                                    313 CCCGCTGGCCGCCTGCTCTACCCCTACCCCTGGCTGGCTTGGCCTTCACGACCACACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGUI2420 1084 bp DNA ROD 14-DEC-1995
Cricetulus griseus mitochondrial benzodiazepine receptor (MBR)
gene, partial cds.
U12420
                                                                                13 TCTCCGCTGGTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGG 72
                  Gaps
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/product="mitochondrial benzodiazepine receptor"
/db_xref="PID:g1039378"
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join(<1. .40,1030. .>1084)
/gene="MBR"
                 ö
Best Local Similarity 0.3%; Pred. No. 1.82e-08; Matches 1; Conservative 203; Mismatches 165; Indels
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/organism="Cricetulus griseus"
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Krueger, K.E.
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/translation="WPPIFFGARQMGWALADLLLVSGVATATTLA"
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Pred. No. 3.04e-07;
0; Mismatches 2; Indels
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279 c 302 g 25
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657. .736
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162. .300
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 n.a. database search, using Smith-Waterman algorithm п.а. MPsrch_nn MasPar time 830.75 Seconds 1309.640 Million cell updates/sec Tue Jul 21 15:37:35 1998; Run on:

Tabular output not generated.

>US-09-047-652A-2 (1-652) from US09047652A.seq 652 Title:

1 CCACGGCGAGGTCTCCGCT.......GTTCTTGGAACATGGAATTT GGTGCCGCTCCCAGAGGCGA......CAAGAACCTTGTACCTTAAA Description: Perfect Score: N.A. Sequence: Comp:

652

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 457396 seqs, 834342348 bases Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

emb154 1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om 7:em_ov 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_v1 genbank106 Database:

13:9b_ba 14:9b_htg 15:9b_in 16:9b_om 17:9b_ov 18:9b_pat 19:9b_ph 20:9b_pl 21:9b_pr1 22:9b_pr2 23:9b_ro 24:9b_st 25:9b_sy 26:9b_un 27:9b_v1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 10.376; Variance 5.505; scale 1.885 Statistics

SUMMARIES

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Result	Ų	Query					
Š.	. Score	Match	Match Length DB	BB	O C	Description	Pred. No.
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	2 542	83.1	639	21	HUMBENZA	Human peripheral benzo	0.00e+00
	3 403	61.8	684	21	HSPBR4	Human peripheral benzo	1.05e-287
υ	4 403	61.8	160559	14	HS1191B2		1.05e-287
	5 402	61.7	4258	21	HSU12421		6.58e-287
	6 384	58.9	152843	14	HS526114		1.53e-272
	7 290	44.5	821	10	BOVPBRIBP	Calf peripheral-type b	7.45e-198
	8 284	43.6	626	23	MUSMPBR	Mouse peripheral-type	4.13e-193
	9 278	42.6	781	23	RATPKBSX	Rat peripheral-type be	2.27e-188
7	0 276	42.3	856	23	MUSPIBR	Mouse mRNA for periphe	8.60e-187
7	1 128	19.6	645	21	HSPBR3	Human peripheral benzo	8.17e-72
1	2 115	17.6	3434	23	RATPTB2R02	Rat peripheral-type be	4.95e-62
7	3 108	16.6	487	77	HSPBR2	Human peripheral benzo	8.35e-57
1	39	6.0	7218	18	166494	Sequence 14 from paten	1.90e-08
1	5 37	5.7	1084	23	CGU12420	Cricetulus griseus mit	3.15e-07

	M36035 M36035 9184333 peripheral benzodiazepine receptor. Human cDNA to mRNA. Homo sapiens Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821) Riond, J. Mattel, M.G., Kaqhad, M., Dumont, X., Guillemot, J.C., Le Fur, G., Caput, D. and Ferrara, P. Fur, G., Caput, D., Riond, Sanofi Elf Bio-Recherches, BP13 Furd, J. and J. Fur, G., Caput, P. Fur, G., Caput, D. Fur, G., Caput, D. Fur, G., Caput, D. Fur, G., Sanofi Elf Bio-Recherches, BP13 Fur, G., Sanofi Elf Bio-Recherches, BP13 Fur, G., Caput, P. Fur, G., Caput, D. Fur, G., Caput, D. Fur, G., Caput, D. Fur, G., Caput, D. Fur, G., Caput, B. Fur, G., Caput, D. Fur, G., Caput, J. Fur, G., Caput, J.
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                                                                                 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 639)
Lin, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.
The human peripheral benzodiazepine receptor gene: cloning a characterization of alternative splicing in normal tissues apatient with congenital lipoid adrenal hyperplasia Genomics 18 (3), 643-650 (1993)
                                                       Gaps
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Eukaryotae; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 684)
Lin, D., Chang, Y. J., Strauss, J.F. and Miller, W.L.
The human peripheral benzodiazepine receptor gene: cloning and
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Homo sapiens DNA.
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/db_xref="PID:g488425"
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characterization of alternative splicing in normal tissues and in patient with congenital lipoid adrenal hyperplasia Genomics 18, 643-650 (1993) 94140364
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Submitted (23-MAR-1998) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
1191B2; HTGS phase 1.
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160559)
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/tissue_lib="placenta"
join(L21952:195..376,L21953:224..362,164..352)
/codon_start=1
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Pred. No. 1.05e-287;
0; Mismatches 3; Indels (
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                                                                                                                                                                                                  /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                       Location/Qualifiers
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Best Local Similarity 99.3%;
Matches 406; Conservative
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IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 ns separate segments. Unfinished sequence: bx119182 Contig_ID: 01503 acc—Length: 1031 bp Unfinished sequence: bx119182 Contig_ID: 01006 acc—Length: 1183 bp Unfinished sequence: bx119182 Contig_ID: 00094 acc—Length: 12000 unfinished sequence: bx119182 Contig_ID: 00094 acc—Length: 1354 bp Unfinished sequence: bx119182 Contig_ID: 00094 acc—Length: 3574 bp Unfinished sequence: bx119182 Contig_ID: 00095 acc—Length: 3574 bp Unfinished sequence: bx119182 Contig_ID: 00095 acc—Length: 3574 bp Unfinished sequence: bx119182 Contig_ID: 00095 acc—Length: 215 bp Unfinished sequence: bx119182 Contig_ID: 00095 acc—Length: 215 bp Unfinished sequence: bx119182 Contig_ID: 0145 acc—Length: 319 bp Unfinished sequence: bx119182 Contig_ID: 0185 acc—Length: 515 bp Unfinished sequence: bx119182 Contig_ID: 0182 acc—Length: 510000 unfinished sequence: bx119182 Contig_ID: 0182 acc—Length: 51000 unfinished sequence: bx119182 Contig_ID: 0182 acc—Length: 10000 unfinished sequence: bx119182 Contig_ID: 0183 acc—Length: 10000 unfinished sequence: bx119182 Contig_ID: 0183 acc—Length: 10000 unfinished sequence: bx119182 Contig_ID: 010000 unfinished sequence: bx119182 Contig_ID: 0100000 unfinished sequence: bx119182 Contig_ID: 010000 unfinished seq
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/organism="Homo sapiens"
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/chromosome="22"
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/product="mitochondrial benzodiazepine receptor"
/db_xref="pib:9529946"
/rbaslation="mappwybamerilapsLGCFVGSRFVHGEGLRWYAGLQKPSWHP
PHWVLGPWGTLYSAMGYGSYLVWKELGGFFEKAVVPLGLYTGQLALNWAWPPIFFGA
RQMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAFTTILNYCVWRDNHG
                                                                                                                                                                                                                                                                                                                                                       Krueger, K. E.

Mineter Submission

Birner (19-701-1994) Karl E. Krueger, Dept. of Cell Biology,

Georgetown University School of Medicine, Washington, DC 20007, USA

Location/Qualifiers
                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 2080 to 3683)
Yakovlev, A. G., Ruffo, M., Jurka, J., and Krueger, K.E. Comparison of repetitive elements in the third intron of human and Gene 155 (2), 201-205 (1995)
                                                                                                                                     HSU12421 4258 bp DNA PRI 14-DEC-1995
Human mitochondrial benzodiazepine receptor (MBR) gene, complete
71540 CCAGGCCAGGTAGGGGTAGAGCAGGCGGGCGGCCAGCGGGCTCACCTGGTACCAGGCCAC 71599
              /evidence=experimental
/product="mitochondrial benzodiazepine receptor"
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                                                    join(129. .310,1941. .2079,3684. .3872)
/gene="MBR"
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/db_xref="taxon:9606"
/map="22q13.3"
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1941. .2079
/gene-"MBR"
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/note="4 Alus"
/rpt_family="Alu"
3497. .3581
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/gene="MBR"
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/gene="MBR"
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Direct Submission
Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfiliahed and does not necessarily
represent the correct sequence. Work on the sequence is in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with foreign sequence from E.coll, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: dJ556114 Contig_ID: 00003 Length: 15560 bp Unfinished sequence: dJ526114 Contig_ID: 00229 Length: 791 bp Unfinished sequence: dJ526114 Contig_ID: 00240 Length: 810 bp Unfinished sequence: dJ526114 Contig_ID: 00248 Length: 750 bp Unfinished sequence: dJ526114 Contig_ID: 00250 Length: 763 bp Unfinished sequence: dJ526114 Contig_ID: 00263 Length: 763 bp Unfinished
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
526I14; HTGS phase 1.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152843)
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/product="mitochondrial benzodiazepine receptor"
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Pred. No. 6.58e-287;
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/rpt_family="MIR"
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/number=4
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larity 99.8%;
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Pred. No. 1.53e-272;
0; Mismatches 5; Indels 3;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="526114"
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Best Local Similarity 98.1%;
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/product="benzodiazepine receptor isoquinoline binding protein"
/db_xref="plo-gi63489"
/db_
                                                                                                                                                                                                                                                                                receptor isoquinoline binding
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Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases) 1 to 821)
Parola,A.L., Stump,D.G., Pepper,D.J., Krueger,K.E., Regan,J.W. and Laird,H.E.II.
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        134532
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benzodlazepine receptor 1soquinoline binding protein.
Calf adrenal gland, cDNA to mRNA.
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Indels
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Pred. No. 7.45e-198;
O; Mismatches 80;
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91310699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9913"
/dev_stage="calf"
/tissue_type="adrenal g-
/tissue_lib="of David R1
67.806
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1. .821
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67. .576
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/gene="PBR/IBP"
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Local Similarity 82.3%;
les 382; Conservative
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/db_xref="PID:9309442"
/db_xref="PID:9309442"
/ranslation="MPESWPAWGLTLVPSLGGFWGAYFVRGEGLRWYASLOKPSWHP
PRWTLAPIWGTLY_SAMGYGGYIVWKELGGFFEDDAMVPLGLYTGQLAWWAWPPIFFGA
RQMGWALADILLLVSGWATATTLAWHRVSPPAARLLYPYLAWLAFATVLNYYWRDNSG
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                                                                                                                                                       MUSMPBR 626 bp mRNA ROD 27-JUL-1994
MOUSE peripheral-type benzodiazepine receptor mRNA, complete cds.
L17306
                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                     1 (bases 1 to 626)
Garnier, M., Dimchev, A.B., Boujrad, N., Price, J.M., Musto, N.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 TGGAAAGACTGGGAGGCTTCACAGAGAAGGCTGTGGTTCCCCTGGGCCTCTACACTGGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTGGCCGATCTTCTGCTTGTCAGTGGGGTGGCGACTGCCACAACCCTGGCTTGGCAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTTGGTGGATCTCCTGCTGGTCAGTGGGGCGGCGCGCACCACACACGTGGCCTGGTAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 ACACTGGCTCCCATCTGGGGCACACTGTATTCAGCCATGGGGTATGGCTCCTACATAGTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 TGGAAAGAGCTGGGAGGTTTCACAGAGGACGCTATGGTTCCCTTGGGTCTCTACACTGGT 291
            563
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 GCACCAGGTGAGCCCGCCGGCTGCCTGCTGTACCCGTACCTGGCCTGGCTTGGCCTTT
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Pred. No. 4.13e-193;
0; Mismatches 90; Indels
                                                                                             564 GCICICGGAAIGAGGACGCCICGCCCTCCGAGGACTGCAGCCGC 607
                                                                                                          benzodiazepine receptor.
Mus musculus mouse testis tumor cDNA to mRNA.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                 1.626
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="MA-10"
/cell_type="leydig"
/tissue_type="mouse testis tumor"
31.540
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Similarity 80.6%;
374; Conservative
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MEDLINE
FEATURES
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Paripheral-type benzodiazepine receptor.

Rat adult adrenal cortex, cDNA to mRNA.

Rattus norvegicus
Eukaryotes; mitochondrial eukaryotes; Wetazoa; Chordata;
Eukaryotes; mitochondrial eukaryotes; Wetazoa; Chordata;
Wurinae; Rattus.

Murinae; Rattus.

1 (bases 1 to 781)
1 (bases 1 to 781)
2 (bases 1 to 781)
Molecular cloning and expression of cDNA encoding a peripheral-type benzodiazepine receptor
Disol. Chem. 264, 20415-20421 (1989)
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/db_xref="PID:9206162"
/db_xref="PID:9206162"
/translation="MSQSWVDAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
PRWTLAPIWGTLYZBANGYGSYIIWKELGGFTEEAMYPLGLYTGQLALWWAWPPIFFGA
RQMGWALVDLMLVSGVATATILAWHRVSPPAARLLXPYTAWLAFATMLNYYWRDNSG
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                                                                                                                                                                                                                                                                                                      RATPKBSX 781 bp mRNA ROD 12-JUN-1992
Rat peripheral-type benzodlazepine receptor (PKBS) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 CAGCIGGCICIGAACIGGGCAIGGCCCCCCAICITICIIIGGIGCCCGGGAGAIGGGCIGG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 GGTGAGGGCCTCCGCTGGTATGCTAGCTTGCAGAAACCCTCCTGGCATCCGCCTCGCTGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 ACACTCGCTCCCATCTGGGGCACACTGTATTCGGCCATGGGGTATGGCTCCTACATAATC 235
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer readable copy of sequence [1] kindly provided by Krueger K.E., 20-SEP-1989.
Location/Qualifiers
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Pred. No. 2.27e-188;
0; Mismatches 76;
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35. .544
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Best Local Similarity 82.3%;
Matches 354; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 645)
Lin,D., Changy,J., Strauss,J.F. and Miller,W.L.
The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and spatient with congenital lipoid adrenal hyperplasta Genomics 18, 643-650 (1993)
                                                                                                                                                                                                                                                                                                                                                245 GCCTTGGTGGATCTCCTGCTGGTCACTGGTGGCGGCGGCCACTACCGTGGCCTGGTAC 304
                                                                                                                                                                                                                                                                                                                                                                                                     CGAGTGAGCCCGCCCGCTGCCCGCTTGCTGTACCCTTACCTGGCCTGGCTTGTTTGCC 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                         223 GGTACGGCTCCTACCTGGTCTGGAAAGAGCTGGGAGGCTTCACAGAGAAGGCTGTTGGTT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             benzodiazepine receptor; peripheral benzodiazepine receptor.
3 of 4
                                                                                                                                                                                                                                                                    65 GTGCTGGGCCCTGTCTGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCCTACCTGGTC
                 GGCGAGGGCCTCCGGTGGTATGCTAGCTTGCAGAAACCCTCTTGGCATCCGCCTCGCTGG
                                                       5 GGCGAGGGTCTCCGCTGGTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGG
                                                                                            207 ACACTGGCTCCCATCTGGCCAACACTGTATTCAGCCATGGGGTATGGCTCCTACATAGTC
                                                                                                                                                                        TGGAAAGAGCTGGGAGGTTTCACAGAGGACGCTATGGTTCCCTTGGGTCTCTGTACACTGGT
                                                                                                                                                                                                                                               327 CAGCTGGCTCTGAACTGGGCGTGGCCCCCCATCTTCTTTGGTGCCCGGCAGATGGGCTGG
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/product-"peripheral benzodiazepine receptor"
177 c 192 g 138 t
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L21953
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Pred. No. 8.17e-72;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .645
/organism="Homo sapiens"
/organism="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
224. .362
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Best Local Similarity 98.6%;
Matches 140; Conservative
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Homo sapiens
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ACCESSION
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Submitted (15-OCT-1993) to the DDBJ/EMBL/GenBank databases. Shigeru
Taketani, Kansai Medical University, Dept. of Hygiene; 10-15
Funizono-cho, Moriguchi, Osaka 570, Japan
(Tel:06-992-1001(ex.2504), Fax:06-992-3522)
Submitted (15-Oct-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="peripheral-type benzodiazepine receptor"
/db_xref="PID:d1005281"
/db_xref="PID:q484054"
/danslation="MESWYPENGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHP
PRWTLAPIWATLYSAMGYGSYIVWKELGGFTEDAMVPDGLYTGOLALWWAWPPIFFGA
RQMGWALADLLLVSGVATATLAWHRVSPPAARLLYPYLAWLAFATVLNYYWRDNSG
                                                                                                                                                                                                                                                                                                                                                                                                 peripheral-type benzodiazepine receptor.
Mus musculus cell-line erythroleukemia (library: lambda gtll) cDNA
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Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                       476 ACCATGCTCAACTACTATGTATGGCGTGATAACTCTGGTCGGCGAGGGGGCTCCCGGCTC 535
245 GCCTTGGTGGATCTCCTGCTGGTCAGTGGGGCGGCGGCAGCCACTACCGTGGCCTGGTAC 304
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1 (bases 1 to 856)

Taketani,S., Kohno,H., Okuda,M., Furukawa,T. and Tokunaga,R. Induction of peripheral-type benzodiazepine receptors during differentiation of mouse erythroleukemia cells. A possible involvement of these receptors in heme blosynthesis 3. Biol. Chem. 269, 2527-7531 (1994)
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Pred. No. 8.60e-187;
0; Mismatches 94; Indels
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/clone_lib="lambda gtil"
66. .575
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/db_xref="taxon:10090"
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Kansai Medical University
1-Fumizonocho, Moriguchi
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Matches 370; Conservative
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Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 487)
Lin, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.
The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and spatient with congenital lipoid adrenal hyperplasta Genomics 18, 643-650 (1993)
                                  105 GGTACGGCTCCTACCTGGTCTGGAAAGAGCTGGGAGGCTTCACAGAGAAGGCTGTGGTTC 164
                                                                                                                                                                                                                                                                               benzodiazepine receptor; peripheral benzodiazepine receptor.
2 of 4
                                                                                                                                                                                                 HSPBR2 487 bp DNA PRI 20-M
Human peripheral benzodiazepine receptor gene, exon 2.
L21952
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1. 487
/organism="Homo sapiens"
/db_xref="taxon:9606"
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1491 c 1486 g
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Best Local Similarity 100.0%;
Matches 108; Conservative
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/product="peripheral-type benzodiazepine receptor"
/product="peripheral-type benzodiazepine receptor"
/db_xref="plD:9206480"
/translation="MSOFWANGLTLVPSLGGFWGAXFVRGEGLRWYASLQKPSWHP
PRWTLAPIWOTLYSAMGYGSYIIWKELGGFFEEAWYPLGLYTGQLALNWAWPPIFFGA
RQMGWALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAFATWLNYYWRDNSG
                                                                                                                                                                                                                                                                                                                1 (bases 1 to 3434)
Sprengel, R., warner, P., Seeburg, P.H., Mukhin, A.G., Santi, R.M., Grayson, D.R., Guidotti, A. and Krueger, K.E.
Molecular Cloning and Expression of cDNA Encoding a Peripheral-type Benzodiazepine Receptor
J. Biol. Chem. 264, 20415-20421 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure of the rat gene encoding the mitochondrial benzodiazepine
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Casalotti.5.0., Pelala,G., Yakovlev,A.G., Csikos,T., Grayson,D.R.
and Krueger,K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HI site, leaving a gap of about
                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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     164 CCCCTGGGCCTCTACACTGGCCAGCTGGCCCTGAACTGGGCATGGCCCCCCATCTTTT 223
                                                                                                                                         RATPTBZR02 3434 bp DNA ROD 25-JAN-1993 Rat peripheral-type benzodiazepine receptor gene exons 2-4, complete cds.
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Pred. No. 4.95e-62;
0; Mismatches 13; Indels
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1. 343m="Rattus norvegicus"

/organism="Rattus norvegicus"
/db_xref="faxon:10116"
/dev_stage="adult"
order(M95864:1273. .1462,1. .1094)
                                                                                                                                                                                                                                                                    Rattus norvegicus (strain Wistar) Adult DNA
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/note="putative"
                                       Gene 121, 377-382 (1992)
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/number=3
2066. .2924
/number=3
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Best Local Similarity 90.8%;
Matches 128; Conservative
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1. .3350
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/tissue_type="placenta"
/tissue_lib="placenta"
166. .376
/product="peripheral benzodiazepine receptor"
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                                                                                                                   Length 487;
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                                                                                                                Score 108; DB 21; Length 48
Pred. No. 8.35e-57;
0; Mismatches 0; Indels
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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Sequence 14 from patent US 5670367.
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Search completed: Tue Jul 21 15:51:40 1998
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Submitted (19-JUL-1994) Karl E. Krueger, Dept. of Cell Biology,
Georgetown University School of Medicine, Washington, DC 20007, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 41 to 1029)
Yakovlev.A.G., Ruffo,M., Jurka,J. and Krueger,K.E.
Comparison of repetitive elements in the third intron of human and gene 155 (2), 201-205 (1995)
                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chinese hamster.
Cricetulus griseus
Eukaryotes; Michochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Cricetinae; Cricetulus.
                                            13 CCCTGTCTGGGGCACGCTCTACTCACCATGGGGTACGGCTCCTACCTGGTCTGGAAAGA 132
                                                                                                                                                                                    133 GCTGGGAGGCTTCACAGAGAAGGCTGTGGTTCCCCTGGGCCTCTACACTGGGCCAGCTGGC 192
                                                                                                                                                                                                                                                        193 CCTGAACTGGGCATGGCCCCCCATCTTTGGTGCCCGACAATGGGCTGGGCCTTGGT 252
                                                                                                                                                                                                                                                                                                                    253 GGATCTCCTGCTGGTCAGTGGGGGGGGGGGCAGCTACCGTGGCCTGGTACCAGGTGAG 312
                                                                                                                                                                                                                                                                                                                                                                      CGU12420 1084 bp DNA ROD 14-DEC-1995
Cricetulus griseus mitochondrial benzodiazepine receptor (MBR)
9ene, partial cds.
U12420
                                                                        13 TCTCCGCTGGTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGG 72
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="mitochondrial benzodiazepine receptor"
join(<1. .40,1030. .>1084)
/gene="MBR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=2
/product="mitochondrial benzodiazepine receptor"
/db_xref="PID:g1039378"
                 ö
                 Indels
Best Local Similarity 0.3%; Pred. No. 1.90e-08; Matches 1; Conservative 203; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1084
/organism="Cricetulus griseus"
/db_xref="taxon:10029"
/clone_lib="PCR of genomic DNA"
/cell_line="V79"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence-experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MBR"
<1
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Krueger, K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MBR"
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1. .1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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ORGANISM
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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KEYWORDS
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/product-"mitochondrial benzodiazepine receptor"
279 c 302 g 250 t
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/translation="WPPIFFGARQMGWALADLLLVSGVATATTLA"
                                                                                                                                                                                                                                                        Length 1084;
                                                                                                                                                                                                                                                        Score 37; DB 23; Length 108
Pred. No. 3.15e-07;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              /evidence-experimental
162. 300
/rpt_family-"B1"
340. 422
/rpt_family-"B1"
657. 736
/rpt_family-"B1"
/gene-"MBR"
/number-4
           41. .1029
/gene="MBR"
/number=3
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.1%;
Matches 39; Conservative
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                                                                 repeat_region
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 108.29 Seconds 766.833 Million cell updates/sec Tue Jul 21 15:25:04 1998; Run on:

Tabular output not generated.

>US-09-047-652A-1 (1-652) from US09047652A.seq 652 Description: Perfect Score:

1 CCACGGCGAAGGTCTCCGCT........GTTCTTGGAACATGGAATTT 652 GGTGCCGCTTCCAGAGGCGA.........CAAGAACCTTGTACATAAA N.A. Sequence: Comp:

TABLE default Scoring table:

Gap 6

Dbase 0; Query 0 •• STD Nmatch

176886 segs, 63680241 bases x 2

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq31-2 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 7:part27 28:part28 29:part29 30:part30 31:part31 33:part33 34:part34 35:part35 36:part36 37:part37 Database:

Variance 5.444; scale 1.565 Mean 8.518; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

.81e-0	8	•	6.81e-05	•	•	•	7.17e-04	7.17e-04	•	•	•	7.17e-03	7.17e-03	2.22e-02	\sim	2.22e-02		6.77e-02	6.77e-02	6.77e-02	7	2.03e-01	8	$^{\circ}$	٥.	σ.	96.	ø	ō.	96.
Generic DNA sequence	Generic DNA sequence	Human endothelin-1 an	Human endothelin-1 an	Generic DNA sequence	Human interleukin 8 a	Generic DNA sequence	Generic DNA sequence	Chymase antisense oli	Generic DNA sequence	Generic DNA sequence	Human MDNCF antisense	Generic DNA sequence	Human IL6 antisense o	Generic DNA sequence	Human interleukin 8 a	HCV envelope region n	Human IL5 antisense o	Human endothelin ETA	Human IL6 antisense o	Chymase antisense ol1	e nitric oxi	Human RANTES antisens	Human MDNCF antisense	Substance P antisense	Substance P antisense		DC43 TSAR library gen	ular cell	Human defensin 1 anti	Substance P receptor
970466	070470	$\overline{}$	T76405	070470	T76363	070473	070466	T76452	970471	070473	T76270	070471	T76233	070472	T76363	035072	T76219	642	2	T76452	T76527	T76307	22	643	σ	T76184	m	T76152	62	T76445
12	17	31	31	12	32	12	13																							
114	114	178	178	114	172	114	114	190	114	114	168	114	128	114	172	565	8	125	128	190	379	162	168	250	250	70	74	130	147	264
6.4	4.9	4.9	4.9	4.8	4.8	4.6	4.6	4.6	4.4	4.4	4.4	4.3	4.3	4.1	4.1	4.1	4.0	4.0	4.0	4.0	٠	٠	•	•	•	•	٠	3.7	•	3.7
32	32	32	32	31	31	30	30	30	29	29	59	28	28	27	27	27	56	26	26	26	56	25	25	25	25	24	24	24	24	24
15	16	17	18	19	20	71	22	23	24		56		28			31				35	36	37	38	39	40	41	42	43	44	45
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Claim 1: Page 1068; 2245pp; Japanese.

Claim 1: Page 1068; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7817 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
form various human deform 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
if from various human tissues; synthesis of cDNA was initiated from the
if of man appeared sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
cecognising different cell types.
Sequence 272 BP; 43 A; 78 C; 86 G; 51 T; 11-NOV-1995.
11-NOV-1994; J01916.
12-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(AMATS)/ MATSUBARA K.
(OKUBA) OKUBO K.
MATSUBARA K.
(OKUBA) OKUBO K.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues 727-AUG-1996 (first entry)
Human gene signature HUMGS03766.
Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
HOMO Saplens.
W09514772-A1. 멾 standard; cDNA to mRNA; 272 122195

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20-MAR-1988; 105163.
20-MAR-1988; US-034819.
23 - MAR-1988; US-034819.
26 SUSO) SUOWEN SOKERI O'.
27 Ichtovasar B'. Knowles J'. Koivula A, Bamford J'. Reinikainen T;
28 WPI; 88-279927/40.
28 MPI; 88-279927/40.
29 Introducing random point mutations into nucleic acods -
29 Isclosure; p: English.
29 Disclosure; p: English.
29 Single stranded template, annealing a primer, elongation, and point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of pax molecules which terminate at all possible nucleotide positions within a specified region. The possible nucleotide positions within a specified region. The reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be transcriptase and the molecules are completed to forms that can be maplified and then expressed in a suitable host-vector system.
20 maplified and then expressed in a suitable host-vector system.
21 The sequence covers all 176 diffit base substitutions, most of which contained and MBP.
21 Secales of MBP.
21 A. 77 MPI T. 108 Others.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 CAGCTGCCCAGTGTAGAGGCCCAGGGGAACCACAGCCTTCTGTGTGAAGCCTCCAGGCTC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                      86 ymrttthhyrrmrbnvyrdyn-rsdaaawyccyrrsvkydccynachhddhyvybbbvyn 144
                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 41; DB 1; Length 204;
larity 7.7%; Pred. No. 1.04e-09;
Conservative 60; Mismatches 35; Indels
/*tag=
                                                                                                                                                                                                                                                                                                                                                     204 BP;
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-571911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                         314 CCGCTGGCCGCCCGCCTGCTCTACCCTGGCCTGGCTGGCCTTCACGACCACTC 373
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14 A consists of nucleotides 5-95 of MK14
(Q5135). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 % 17 C; 15 G; 4 T;
                                                                           1 gatetectgetggteagtgggggggggggeage-actaccgtggcetggtaccaggtgage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N81164;
08-NOV-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA: WHI; 93-37884448. New oligo:nuclectide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                  Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 9; Length 91;
Pred. No. 2.23e-11;
46; Mismatches 4; Indels
                Score 238; DB 20; Length 27; Pred. No. 3.02e-134; 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/function=multiple cloning site
187..204
                                                                                                                                                                                                                                                                                                              240 tggccgtnangttttaatgaccantgggnctg 271
                                                                                                                                                                                                                                                                                                                                        494 rescenteacerricareaceacressers 525
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                                                                                                                                                                                                                                                                                                                                                                             .r. 2
Q51746 standard; cDNA; 91 BP.
Q51746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.7%;
Best Local Similarity 3.8%;
Matches 2; Conservative
                Query Match
Best Local Similarity 92.3%;
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
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11 T; 108 Others;

17 G;

47 C;

21 A;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 3; Page 14; 23pp; English.
Oligiouschedide probe MK14-A consists of nucleotides 5-95 of Oligiouschedide probe MK14-A consists of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Seequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                 31-WAY-1994 (first entry)
Oligonuclectide probe MK14-A
Oligonuclectide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 9; Length 91;
Pred. No. 3.68e-09;
42; Mismatches 8; Indels
145 vhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                87
                             24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                   T
Q51746 standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 10.7%;
Matches 6; Conservative
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Escherichia coli.
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                                                                                                                                                                                                                                                                  PF 01-FEB-1993; US-013416.

R 10-FEB-1993; US-013416.

R 20-DEC-1993; US-176500.

PR 30-DEC-1993; US-176500.

PR 31-AN-1994; US-189331.

PR 4 (UVNC-) UNIV NORTH CAROLINA.

FOWIKES DM KAY BK;

NWIT; 94-279739/34.

R P-FSDB; R65150 and R65151.

PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain proteins or peptides. This generate can also be servered as follows: X(NNB) English.

C 470465 is a general DNA sequence used to generate random TSAR (Totally DISCIOSURE) as general can also be represented as follows: X(NNB) English.

C 570465 is a general DNA sequence used to generate same as X) that are not specified further. Other general sequences are shown in 070466-68.

C 670465 is a general content of the sequences are shown in 070466-68.

C 700465 is a reconcatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a fiffinity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with a fiffinity for a ligand and a second effector peptide portion that is comprising the unpredicted or variant residues; These residues confirmationed confermational regidity to the peptides. The TSARS or comprasis comprising a TSAR binding domain can be used in vivo to confer some degree of conformational rigidity to the specific target or on the colliver a chemically or biologically active moister, eg metal ion, compans, comprising a TSAR binding domain can be used in vivo to confer sell righty and process and partibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody processes are anally characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                 Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 CTCTGTGAAGCCTCCCAGCTCTTTCCAGACCAGGTAGGAGCCGTACCCCATGGCTGAGTA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
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                                                                                                                                                                          /*tag= a
/note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 12; Length 114 Pred. No. 5.38e-07; 33; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 direct and rapid detection in a
                                                                                                                                           Location/Qualifiers
             r 5
Q70465 standard; DNA; 114 BP.
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N81164 standard; DNA; 204 BP
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llarity 4.5%;
Conservative
                                                       (first entry)
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/*tag=
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                                       070465;
05-APR-1995
                                                                                                                                                            misc_feature
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                                                                                                                               Synthetic.
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            RESULT
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Introducing random point mutations into nucleic acods -

"Introducing random point mutations into nucleic acods -

"Introducing random template, annealing a primer, elongation,

"Introducing random template of molecules and screening.

"Introducing random templation of molecules and screening.

"Introducing mutations were introduced into the alpha fragment of

"Introducing point mutations were introduced into the alpha fragment of

"Interpolate a populate and an oligonucleotide was hybridised to

"It to generate a populo DNA molecules which terminate at all

possible nucleotide positions within a specified region. The

"It to generate a populations within a specified region. The

"It to generate and an oligonucleotide as primers for

"It cranscriptase and the molecules are misincorporated by the

"In reverse transcriptase and the molecules are completed to forms that can be

"The sequence covers all 176 difft base substitutions, most of which

"See also P80575."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 hyrrmrbnvyrdyn-rsdaaawyccyrrsvkydccynachhddhyv-ybbbvynvhnhnn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CTGGTACGCCGGCCTGCAGAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGGCCCTGT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 94-27973974.
Identifying proteins or peptide(s) which bind a ligand - by
screening a recombinant vector library expressing fusion proteins
comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "this sequence represents '2'; 2 can be a
sequence of 6,9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 Others;
                                                                                                                                                                                          05-MAY-1988: 105163.
30-MAK-1988: 105163.
03-APR-1987: US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 204;
Pred. No. 5.38e-07;
53; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCCTACCTGGTC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 T;
                                                                 /function=multiple cloning site 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 G;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 C;
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comments)
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 15.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                             19..69
/*tag= a
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/*tag=
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30-DEC-1993;
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                          misc_feature
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07-APR-1995
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                                                                                                          primer_bind
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CC (7046) is a generic DNA sequence used to generate random TSAR peptide CC This generic formula can be represented as follows: X(TGC)(NNB)10- (TGC)(NNB)4(TGC)Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. This sequences are shown in Q70465-68. Other specific peptides that are cloverleaf in structure. Other generated by these generic sequences are shown in R65150-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. CC contains 2 or 4 cysteine residues positioned in, or flanking, the upredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compension conformational rigidity to the peptides. The TSARs or compension or margine decine and to deliver a chemically or belonged to reazyme, to the specific target or on the cell. They can also replace the function of macromolecules, eq. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma for a reason of the result of the residue activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; page 35: 25pp; English. Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)17(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ccgcrggracgccggccrgcagaagcccrcgrggcacccgccccacrgggrgcrgggccc 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 12; Length 114;
Pred. No. 1.83e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Mismatches 73; Indels
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//*tag= this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection in a screening process.
Sequence 114 BP; 0 A; 4 C;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNIC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI; 94-279739/34.
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Q70468 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4%;
ilarity 6.3%;
Conservative
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Generic DNA sequence to ger
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/*tag=
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Best Local Similarity
Matches 7; Conser
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01-FEB-1994;
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R65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a filmity for a ligand and a second effector peptide portion that is cementally or biologically active. They may further comprise a linker cementally or biologically active. They may further comprise a linker of peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, e9. metal ion, candiolsotope, peptide, toxin or enzyme, to the specific target or on the coll. They can also replace the function of macromolecules, e9.

Compositional antibodies and therefore circumvent the need composition antibodies and therefore circumvent the need confouncion. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   referring a recombinant vector library expressing fusion proteins recently a recombinant vector library expressing fusion proteins a recombinant vector library expressing fusion proteins a comperition a binding domain and an effector domain proteins by a recombination and an effector domain comperition a planding domain and an effector domain comperition is provided as follows: X(NNB)150. This generic formula can also be represented as follows: X(NNB)1(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)5(CAC)(NNB)6 (CAC)(NNB)6 (CAC)(NN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.2%; Score 34; DB 12; Length 114; Best Local Similarity 2.7%; Pred. No. 6.18e-06; Matches 3; Conservative 34; Mismatches 75; Indels
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
FOWIKES DM, RAY BK; WPI; 94-279739/34.
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Q70472 standard; DNA; 114 BP.
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/*tag=
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01-FEB-1993;
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3.68;

Best Local Similarity

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A O'DEC-1993; US-013410.

PR 31-JAN-1994; US-189331.

PR 31-JAN-1994; US-189331.

PA (UVIC-) UNIV NORTH CAROLINA.

PA (UVIC-) UNIV NORTH CAROLINA.

FOWIKES DW, KBY BK;

ROWINGS DW, KBY BK;

PR 19-279739/34.

PR 27-279739/34.

PR 19-279739/34.

PR 19-279739/34.

PR 19-279739/34.

PR 27-279739/34.

PR 27-279739/37.

PR
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monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 6 A; 12 C; 0 G; 0 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 6.18e-06;
29; Mismatches 71; Indels
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05-APR-1995 (first entry)
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US-176500.
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01-FEB-1994;
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Territy No. 1937.

Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain bisclosure; Page 35: 255pp; English.

Disclosure; Page 35: 255pp; English.

O70467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)11. X and Y are flanking restriction sites (X is not the same as Y) that are contended by these generic sequences are shown in R65151-34. TSARS are concatenated by these generic sequences are shown in R65151-34. TSARS are concatenated beterofunctional proteins or peptides, offinity for a ligand and a second effector peptide portion that is affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide concains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues concents are also residues are also replace to conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ior, or also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.

The TSARs are easily characterised and have designed activity allowing direction of macromolecules.
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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                                                                                                13 TCTCCGCTGGTACGCCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGG 72
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Pred. No. 6.18e-06;
33; Mismatches 75;
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Pred. No. 6.18e-06;
33; Mismatches 75;
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Q70467 standard; DNA; 114 BP
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(UTNC-) UNIV NORTH CAROLINA.
FOWIKES DM, RAY BK;
WHPI; 94-Z79739/34.
P-PSDB; R65153.
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US-176500.
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253 GGATCTCCTGCTGGTCAGTGGGGCGGCGCGCACTACCGTGGCCTGGTACCAGGTGAG 312

DB 12; Length 114;

Score 34;

5.2%;

Query Match

can be

/note- "this sequence represents 'z'; Z sequence of 6, 9 or 12 nucleotides (see comments)"

U00977

Location/Qualifiers 55..60 /*tag= a

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DR FPSDB; R65153.

Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

COMAGO 1s a generic DNA sequence used to generate random TSAR (Totally COMAGO 1s a generic DNA sequences are shown in the same as follows: X(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)12/(NNB)16/TGC)(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(NNB)12/(N
                                     Generic DNA sequence to generate a random ISAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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(UYNC-) UNIV NORTH CAROLINA.
                   (first entry)
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US-176500.
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                 05-APR-1995
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PT comprising a binding domain and an effector domain bischosure; Page 35: 255pp; English.

COMPAGE is a generic DNA Sequence used to generate random TSAR (Totally COMPAGE) and Sequence as follows: x(NNB)11(TCC)(NNB)52(NNB)7(TCC)(NNB)10v. x and Y are flanking restriction sites (X is not the same as Y) that are con specified further. Other generic sequences are shown in 707466-68.

COMPAGE TASARS are concatenated heterofunctional proteins or peptides, other specified that the vector is a binding domain with affailty for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some deegree of conformational rigidity to the peptides. The TSARS or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, corrections or peptide towing a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, corrections or poptide, toxin or enzyme, to the specific target or on the conformation or not macromolecules, eg. metal ion, corrections and polyclonal antibodies and therefore circumvent the need conformation or min vivo antibody correction. The TSARS are easily characterised and have designed activity sequence life BP; 0 A; 2 C; 2 G; 2 T;
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                                                                                                                                                           070468;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
Generic DNA sequence to fiffinity reagent; synthetic; binding domain;
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                           313 CCCGCTGGCCGCCCGCTGTACCTGGCTGGCTGGCTTGACG 364
  DB 12; Length 114;
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/note= "this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
comments)"
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Pred. No. 6.18e-06;
33; Mismatches 75
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKSS DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65154.
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Q70468 standard; DNA; 114 BP.
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larity 3.6%;
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Best Local Similarity
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01-FEB-1994;
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Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. synthetic.
                                                                     130 TITCCAGACCAGGIAGGAGCCGIACCCCAIGGCIGAGAAGAGGGTGCCCCAGACAGGGCC 71
                                   ö
                                                                                                                                          Length 114;
Score 34; Delice 18 Pred. No. 6.18e-06; Virmatches 75; Indels
5.2%; Score 34; DB 12; 2.7%; Pred. No. 6.18e-06;
                                                                                                                                                                                                                                      T 14
Q70469 standard; DNA; 114 BP.
                                   3; Conservative
Query Match
Best Local Similarity
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1D Q7
1D Q7
AC Q7
DT Q7
DE Ge
CKW TS
KW ef
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325 GGGGGCCAGCGGGCTCACCTGGTACCAGGCCACGGTAGTGGCTGCCGCCGCC 274

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RESULT 13 ID Q70467 standard; DNA; 114 BP

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Matches
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CO70469 is a generic DNA sequence used to generate random TSAR peptide CTALS sequence used to generate random TSAR peptide CTALS sequence used to generate random TSAR peptide CTALS generic formula can be represented as follows: X(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction CTALS generates peptides that are not specified further. This sequence generates peptides that are cloverleaf in structure. Other corrected by these general sequences are shown in G70465-68. Other specific peptides concatenated by these general sequences are shown in R65150-54. TSARS are concatenated by these general proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically contains 2 or 4 cysteine residues positioned in, or flanking, the conformational rigidity to the peptides. The TSARS or compsis. Comprising or TAR Dinding domain can be used in vivo to deliver a chemically or biologically active molety, est metal ion, radioisotope, peptide, toxin or a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, est metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace CC and therefore circumvent the need for complex methods of hybridoma complex active and hard and have designed activity allowing direct and rapid
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05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= *this sequence represents '2'; 2 can be
sequence of 6,9 or 12 nucleotides (see
comments)*
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/note="this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
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Pred. No. 2.06e-05;
30; Mismatches 71; Indels
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Location/Qualifiers
55..60
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Sequence 114 BP; 0 A; 4 C
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Q70466 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                             30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 5.6%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55..60
/*tag=
                                                                                                                                                                                                                                    US-013416.
                                                                                                                                                                                                              100977
                                                                                                                                                                                                                                                                                                                                                               WPI; 94-279739/34
  Key
misc_feature
                                                                                                                                                                                                         01-FEB-1994;
01-FEB-1993;
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by screening a recombinate band an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

CO 70466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reasperts) peptides comerate formula can also be represented as follows:XNNB)1(TGC)(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB) CC represented as follows:XNNB)1(TGC)(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB) CC represented as follows:XNNB)1(TGC)(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB) CC represented as follows:XNNB)1(TGC)(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB) CC CO TOPETHOR (INTEL) Sequences are shown in R65151-54. TSARS are concatenated betterofunctional proteins CC are shown in R65151-54. TSARS are concatenated by these generic sequences are shown in R65151-54. TSARS are concatenated by these generic sequences are shown in the chart is chemically or biologically active. They may further comprise a CC linker peptide between the 2 domains. They domain can be used in CC designed so that the expressed peptide contains 2 or 4 cysteine residues confer some degree of conformational rigidity to the peptides. They can also replace the function of macromolecules, eg. The TSARS or compsis. Comprising a TSAR binding domain can comprise or on the cell. They can also replace the function of macromolecules, eg. metal CC monoclonal or polycional antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. CT he TSARS are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 114;
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Pred. No. 6.81e-05;
28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: Tue Jul 21 15:26:57 1998 Job time: 113 secs.
                               01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.9%;
Similarity 8.2%;
9; Conservative
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Best Local Similarity
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tue Jul 21 15:27:14 1998; MasPar time 36.70 Seconds 953.206 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-047-652A-1 (1-652) from US09047652A.seq 652 Description: Perfect Score:

1 CCACGGCGAAGGTCTCCGCT.......GTTCTTGGAACATGGAATTT 652 GGTGCCGCTTCCAGAGGCGA.........CAAGAACCTTGTACATAAA N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

104157 seqs, 26825796 bases x 2 Searched:

Dbase 0; Query 0

STD

Match

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 8.113; Variance 4.783; scale 1.696 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length DB	DB	a	Description		Pred. No.
П	39	6.0	7218	-	US-08-232-	Sequence 14, Ap	Applicati	2.45e-10
2	36	5.5	215		US-08-238-	'n	Applicatio	1.46e-08
m	35	5.4	215	-	US-08-238-	'n	Applicatio	5.58e-08
4	25	3.8	74	7	PCT-US95-1	94	Applicati	1.97e-02
S	25	3.8	81	7	PCT-US95-1	92,	Applicati	1.97e-02
9	24	3.7	74	~	PCT-US95-1	Sequence 94, Ap	Applicati	6.50e-02
7	24	3.7	74	7	PCT-US95-1	100,	Applicat	6.50e-02
∞	24	3.7	75	~	PCT-US95-1	99, A	Applicati	6.50e-02
ص د	24	3.7	81	~	PCT-US95-1	92,	Applicati	6.50e-02
10	24	3.7	81	7	PCT-US95-1	98	Applicati	6.50e-02
11	24	3.7	83	~	PCT-US95-1	97,	Applicati	6.50e-02
12	23	3.5	99	Н	US-08-471-	144,	Applicat	2.10e-01
13	23	3.5	68	Н	US-08-471-	Sequence 143, A	Applicat	2.10e-01
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17	23	3.5	81	~	PCT-US95-1	Sequence 98, Ap	Applicati	2.10e-01
2 18	23	3.5	82	~	PCT-US95-1	97,	Applicati	2.10e-01
19	22	3.4	65	Н	US-08-471-	Sequence 145, A	Applicat	6.61e-01
20	22	~	ď	-	-177-00-011	4 171	4 - 1 - 1	6 610-01

6.61e-01 6.61e-01 6.61e-01 6.61e-01	5.61e-01 2.04e+00 2.04e+00 2.04e+00	2.04e+00 2.04e+00 2.04e+00 2.04e+00		2.04e+00 2.04e+00 6.11e+00 6.11e+00 6.11e+00
144, Applicat 143, Applicat 142, Applicat 1, Applicatio 3, Applicatio	1, Applicatio 1, Applicatio 95, Applicati 95, Applicati 93. Applicati	4 A .	18, Applicati 85, Applicati 1, Applicatio 49, Applicati 84, Applicati	4, Applicatio 23, Applicati 120, Applicat 25, Applicati 25, Applicati 9, Applicatio
Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence		Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence Sequence
US-08-471- US-08-471- US-08-471- US-08-273- US-08-425-	US-08-001- US-07-794- PCT-US95-1 PCT-US95-1	PCT-US95-1 US-08-357- US-08-273- US-08-248-	US-08-136- PCT-US93-0 US-08-136- US-08-306- PCT-US93-0	US-08-195- PCT-US93-0 US-08-133- US-08-300- PCT-US95-1 US-08-368-
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66 69 242 1995	225 225 53 53 65 66	108 242 336	1441 1838 2750 4175	11558 11558 84 84 5399
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22 23 23 23 23 23 23 23 23 23 23 23 23 2	35878	33 33 34 34	3333	0 H G W A G
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Sequence 14, Application US/08232463
Sequence 14, Application:
CORREAL INCEMATION:
CORRESPONDENT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
COURRENT APPLICATION DATE:
COURRENT APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AMG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
RECENCEMONICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-9300
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
  JT 1
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: LABAVITCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
APPLICANT: STORY: Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                     S04 CGIGACGGCCACACACACAAGGGGAGATGGCACCTGCTGGTGCAGCTGCAGGTCCTGGT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 NYGGNNYGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSY-GSSKT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 GGGCCGGGCCACTCTGCCACGCCGCCCACGCCATGCTTGTCCCCGCAT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AMISRNRIGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SSSSVVSRIASCNDKAKKDGNIISSWIIDCCNRIWGVCDIDIIYRVNNDSGHNKYSSANY 66
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                             LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP: 15 A: 8 C: 25 G; 26 T: 141 OTHER.
                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 215;
Pred. No. 1.46e-08;
82; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                    2307E-540
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US-08-238-163-5 STANDARD; DNA; UNC; 215
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CTASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 KSNVSNNCGGGNKRDVSSYANNKCCGSSC 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105-1493
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Release ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08238163 Sequence 5, Application US/08238163 Patent No. 5569830 GENERAL INFORMATION:
NAME: Bastian, Kevin L.
REGIZTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 23071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION ESQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TERE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 13.4%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Steuart Stree
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
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Sequence 5, Application US/08238163

Sequence 5, Application US/08238163

CENERAL INFORMATION:
CHAPLICANT: BENNETT, Alan
APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
CC APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC TITLE OF INVENTION: POWERSED
CC STREET: Steuart Street Tower, One Market Plaza
CC STREET: California
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                                                                                                                                                                                                                                                                                                                                                                                       133 GCTGGGAGGCTTCACAGAGAAGGCTGTGGTTCCCCTGGGCCTCTACACTGGGCAGCTGGC 192
                                                                                                                                                                                                                                                                                                                                                                                                              193 CCTGAACTGGGCATGGCCCCCCATCTTTGGTGCCCGACAAATGGGCTGGGCTTGGT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 GGATCTCCTGCTGGTCAGTGGGGGGGGGGCGCCACTACCGTGGCCTGGTACCAGGTGAG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 CCCGCTGGCCGCCCGCCTGTCTACCTGGCCTGGCCTTCACGACCACCACT 372
                                                                                                                                                                                                                                                                                 Gaps
                                                        TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pT22pt-F1s
SEQUENCE 7218 PF: 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                    DB 1; Length 7218;
                                                                                                                                 Similarity 0.3%; Score 39; DB 1; Length 7218 Similarity 0.3%; Pred. No. 2.45e-10; 1; Conservative 203; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCFUMARE: Patentin Release #1.0, Version #1.25 SCFUMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163 FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .T. 2
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
        LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94105-1493
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                                                                                                                                      Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                             Query Match 3.8%;
Best Local Similarity 9.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.8%;
Best Local Similarity 9.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                    492 GGTGGCCGTCA 502
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                                                                                                                                                                                                                                                                                                              69 GGNNVGAAKTHYYTHTNVSG-ADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
                                                                                                                                                                                                                                                                                                                                           128 ISRNRIGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGIGTKS 187
                                                                                                                                                                                                                                                        9 SSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNY 68
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: Sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                             Score 35; DB 1; Length 215;
Pred. No. 5.58e-08;
81; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 100 PG A COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        T
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION UNUBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                 188 NVSNNCGGGNKRDVSSYANNKC 209
                                                                                                                                                                                                              Ouery Match
Best Local Similarity 12.4%;
Matches 25; Conservative
                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: CYTOGEN COMPORATION
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennia & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                         Score 25; DB 2; Length 74;
Pred. No. 1.97e-02;
20; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTRY: USA

ZIP: 10036
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MISSIOCK, S. Leslie
REGISTRATION NUMBER: 18,872
RESPERENCE/DOCKET NUMBER: 1101-196-228
REGISTRATION NUMBER: 18,872
RESPERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (214) PENNIE
INFORMATION FOR SEQ ID NO: 92:
CENTERNIE GELIA PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 2; Length 81;
Pred. No. 1.97e-02;
20; Mismatches 44; Indels
TELEPHONE: (212) 790-9090
TELEFAX: (512) 869-9741/8864
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DAA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .T 5
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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                   432 GAGIGCCCGGCCCACCAGGGACIGCAGCIGCACCAGCAGGIGCCAICACGCIIGIGAIGI 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                              Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: OCTOGEN COTPORATION
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCE: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
3.7%; Score 24; DB 2; Length 74;
Best Local Similarity 7.7%; Pred. No. 6.50e-02;
Matches 5; Conservative 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILIG DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA ZIP: 1036
                                                                                            .T 6
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 7
PCT-US95-11934-100 STANDARD; DNA; UNC; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 100, Application PC/TUS9511934 Sequence 100, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENUE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                             492 GGTGGCCGTCA 502
                                        70 BNNBNACGCCA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 GGCCA 294
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                                                                                             RESULT
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WPELICANT: Cytogen Corporation

CC TITLE OF INVENTION: Antigen Binding Pertides (Abtides) From Washer On Suburbers: 131

CC TITLE OF INVENTION: Antigen Binding Pertides (Abtides) From Washer On Suburbers: 131

CC CONTRICT: New York Same Same Same Same State: New York ST
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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
 STRANDEDNESS: single
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494 ACCACA 489
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                                                                                                                                                                                                                                                                                                                                                                             432 GAGTGCCCGGCCCACCAGGGACTGCAGCTGCACCAGGAGGTGCCATCACGCTTGTGATGT 491
                                                                                                                                                                                                                                                                                                                                                 Sequence 92, Application PC/TUS9511934
C GENERAL INFORMATION:
C APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
C TITLE OF INVENTION: Peptide Libraries
C NUMBER OF SEQUENCES: 103
C CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
C CTY: New York
C COUNTRY: USA
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                         / Match 3.7%; Score 24; DB 2; Length 75; Local Similarity 6.2%; Pred. No. 6.50e-02; es 4; Conservative 20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1090-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 92:
SEQUIENCE CHARACTERISTICS:
       CURRENT AFFLICATION DATA:

APPLICATION WUBBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLEASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELECAM, (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDENS: single
                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7T 9
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 81 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10036
                                                                                                                                                                                                                                                                                                                                                                                                                                   492 GGTGG 496
                                                                                                                                                                                                                                                                                                                                                                                                         63 BNNBG 67
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                                              O; Gaps
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Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: CYPENDER COMPORATION
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennia & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
IP: 1003A
IP: 1001A
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: TBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA: 20-SEP-1995
CLASSIFICATION OFFER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NUMBER: 1101-196-228
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEFAM: (212) 790-9090
TELEFAM: (212) 790-9090
TELEFAM: (212) 790-9090
TELEFAM: 6141 PENNIE
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPER: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 2; Length 81;
Pred. No. 6.50e-02;
19; Mismatches 41; Indels
Score 24; DB 2; Length 81;
Pred. No. 6.50e-02;
20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                                                                                                                              T 10
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
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Best Local Similarity 9.1%;
Matches 6; Conservative
Query Match 3.7%;
Best Local Similarity 7.7%;
Matches 5; Conservative
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RESULT

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MOLECULE TYPE: DNA
SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .T 13
US-08-471-052A-143 STANDARD; DNA; UNC; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711 ORN:
MEDIUM TYPE: Floppy disk
STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Query Match 3.5%;
Best Local Similarity 9.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                       STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GG 65
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Sequence 144, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.7%; Score 24; DB 2; Length 82; Best Local Similarity 10.1%; Pred. No. 6.50e-02; Matches 7; Conservative 19; Mismatches 43; Indels
                                                                                                                                                                                                                                                         MEDIUM TIPE: FLOPPY GISH
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
PPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
NAME: MISTOCK, S. Lesle
REGISTRATION NUMBER: 1101-196-228
REFERENCE/POCKET NUMBER: 1101-196-228
TELEPHONE: (212) 799-9090
TELEPHONE: (212) 799-9090
TELEFA: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDENESS: Single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 12
US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
                            JT 11
PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
XXXXXX
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135 AGCICTITCCAGACCAGGIAGGAGCCGIACCCCAIGGCIGAGIAGAGCGIGCCCCAGACA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 143, Application US/08471052A
Sequence 143, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOWLKes, D. M.
TILLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin DaTa:
COMPUTERING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin DaTa:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION NUMBER: US/08/471,052A
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION NUMBER: 18/872
REFERENCE/DOCKET NUMBER: 1101-179
CTELECOMMUNICATION INFORMATION:
CTELECOMMUNICATION INFORMATION:
CTELEFAX: 66141 PENNE:
CC TELEFAX: 6141 PENNE:
CC TELEFAX: 6141 PENNE:
CC TELEFAX: 6641 PENNE:
CC SEQUENCE CHARACTERISTICS:
LENGTH: 66 bases
LENGTH: 66 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; Length 66;
Pred. No. 2.10e-01;
18; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE: 06-JUNE-1995
CLASSIPICATION: 530
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Query Match
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Sequence 142, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TILLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
                                                                                                                                                              Query Match 3.5%; Score 23; DB 1; Length 68; Best Local Similarity 13.4%; Pred. No. 2.10e-01; Matches 9; Conservative 18; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STATE: New York
STATE: New York
COUNTRY: U.S.A.
2 IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OCHERING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMUNICATION INFORMATION:
TELEFAX: 212 869-8864/9741
TELEFAX: 212 869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH : 68 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 68 BP; 3 A; 3 C; 5 G; 3 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                              JT 14
US-08-471-052A-142 STANDARD; DNA; UNC; 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MASTOCK, S. LESILE
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 1101-
TELECHONICATION INFORMATION:
TELERAX: 212 869-8864/9741
TELERAX: 66441 PENNIE
INFORMATION FOR SEC ID NO: 142:
SEQUIENCE CHARACTERISTICS:
LENGTH: 69 bases
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C Sequence 100, Application PC/TUS9511934
C GENERAL INFORMATION:
C TILLE OF INVENTION: Peptide Libraries
C TILLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES:
C CORRESPONDENCE ADDRESS:
C ADDRESSE: Pennle & Edmonds
STREET: 1155 Avenue of the Americas
C CITY: New York
C CITY: New York
C COUNTRY: USA
C CITY: USA
                                                    Gaps
                                                    ö
  Score 23; DB 1; Length 69;
Pred. No. 2.10e-01;
17; Mismatches 40; Indels
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COMPUTER: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: BM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CONTREMY APPLICATION NATA:

APPLICATION NUMBER: PCT/US95/11934

FILING DATE: 20-SEP-1995
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PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
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MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
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NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
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TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
Query Match
Best Local Similarity 13.6%;
Matches 9; Conservative
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Release 3.1A Copyright (c)	3.1A John F. Collins, Biocomputing Research Unit. t (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
MPsrch nn n.a n.	a. database search, using Smith-Waterman algorithm		
Tue	21 15:11:50 1998; MasPar time 760.50 Se		
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Statistics: Mean	Mean 10.452; Variance 2.420; scale 4.319	AUTHORS	
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	SUMMARIES		Te.
Result Query No. Score Match	% Query Match Length DB ID Description Pred. No.		THE
	546 15 AA724486 ah99hll.sl Soares NFL 0.00e+00 572 9 AA527126 n770bl2.sl NCL_CGAP_La 0.00e+00	FEATURES	SE H10
4 459 70	13 AA//5/35 Zf31I04.S1 Soares Teta 23 AA161033 Zo58604.S1 Stratagene 13 AA066430	Ø.	source
452 69 7 446 68	10 AA595715 n146e08.si NCI_CGAP_Lu 11 AA543068 nr95f04 si NCI_CGAP_Lu		
8 442 67 9 437 67	8 AA210894 zr90g06.sl NCI_CGAP_GC 11 AA479680 zu43a07.sl Soares ovar		
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obb6c01 s1 NCI_CGAP_GC ob22g01.s1 NCI_CGAP_KI zu43a07.r1 Scarses ovar ad16e07.s1 Scarses ovar ad16e07.s1 Scarses ovar ad36d03.s1 NCI_CGAP_Fr n0136d03.s1 NCI_CGAP_Fr n0136d03.s1 NCI_CGAP_Fr n011602.s1 NCI_CGAP_Br cc15c05.s1 NCI_CGAP_Br cc15c05.s1 NCI_CGAP_Br cc15c05.s1 NCI_CGAP_GC cd15c07.s1 NCI_CGAP_GC cd18c10.s1 NCI_CGAP_GC cd18c10.s1 NCI_CGAP_GC cd18c10.s1 NCI_CGAP_GC s18c10.s1 Stratagene zd177h01.s1 Stratagene zd3g05.s1 NCI_CGAP_L z177h01.s1 Stratagene zd3g05.s1 NCI_CGAP_L z03g05.s1 Scarses sene zc20g05.s1 Scarses sene zc20g05.s1 Scarses sene zd3b012.r1 Scarses sene zd3b012.r1 Scarses sene zd3c609.r1 NCI_CGAP_CC zc51c06.r1 NCI_CGAP_CC zc51c06.r1 NCI_CGAP_CC zc51c06.r1 NCI_CGAP_CC zc51c06.r1 Scarses feta za26609.r1 NCI_CGAP_CC zc51c06.r1 Scarses feta za26609.r1 NCI_CGAP_CC zc51c06.r1 Scarses feta za26609.r1 NCI_CGAP_CC zc51c06.r1 Scarses feta za26c09.r1 NCI_CGAP_CC	
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similar to gb:U12421_cdsl PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
HUMAN);, mRNA sequence.
AA587126
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            Bento
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                                                                                                                                                                                                                                AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACATCACAAGCGTGATGGC
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
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                                                                                                      Length 546;
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                                                                                                      Score 498; DB 15; 1
Pred. No. 0.00e+00;
0; Mismatches 8;
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llarity 98.4%;
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AUTHORS
TITLE
                                                                           SASE COUNT
                                                                                                                                                                                                                                                                                                                                                                            352
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//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Larynx, Vector: Bluescript SK-; Site_1:
ECORI; Site_2: Noi; Cloned unidirectionally. Primer:
0.140 dT. Larynx. 5' adaptor sequence: 5' GAATTCGGCACGAG
3' a' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT
3' Average insert size: 0.9 kb."
//db_xref="taxon:9606"
//clone="InAGE:10892Is"
//clone="InAGE:10892Is"
//tissue_type="larynx"
//lab_host_SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 493; DB 9; Length 572
Pred. No. 0.00e+00;
0; Mismatches 17; Indels
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                         Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 462.
Location/Qualifiers
                                                                                                 www-bio.llnī.gov/bbrp/image/image.html
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Best Local Similarity 96.5%;
Matches 522; Conservative
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Homo sapiens
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zf31f04.sl Soares fetal heart NbHH19W Homo sapiens cDNA clone
378559 3' similar to gb:012421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.
AA775735
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                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 487.
                                                                                                               Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarinini; Hominidae; Homo.
1 (bases 1 to 567)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S. Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU.NCI human,EST Project
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Pred. No. 0.00e+00;
0; Mismatches 12; Indels
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167 c 175 g 98 t 1 other
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/clone_11b="Soares fetal heart NbHH19W'
/sex="unknown"

    .567
    /organism="Homo sapiens"

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al Similarity 96.3%;
522; Conservative
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zo58e04.sl Stratagene pancreas (#937208) Homo saplens cDNA clone Spl102 3' similar to gb:U12421_dsl PERIPHERAL-TYPE BENZODIAZEPINE Alis1033
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Location/Qualiflers
1. 563
/organism="Homo sapiens"
                                                                                                                                                                                                         448
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                                                 412 CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGTGAAGGCCAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotas; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases it of 563)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
CCCACGCCACCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTGGTCGTGAAGGCCAG
                                                                                                                                                                                                         389 GGTAGTGTGACTCGCCCCCCCACTGACCAGCAGGAGATCCACCAAGGCCCAGCCCATTTG
                                                                                                                                                                                                                                                                                                              449 TCGGGCAC-ANAGAAGATGGGGGGCCATGCC-AGTTCAGGGCCAGCTGCCTAGTGTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK WashU-warck EST Project WashU-warck EST Project WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fex: 314 286 1810 Email: estewatson.wustl.edu
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zml4hil.sl Stratagene pancreas (#937208) Homo sapiens cDNA clone
525669 3' similar to gb:012421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RAD65479
g1577104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Email: 314 286 1800 Email: est@watson.wustl.edu WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should you use this clone.
                          7.
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Bukaryotae, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 610)

Hilliari,... (lark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,

Washb-Merck EST Project

Unpublished (1995)
                                                  94
                          Gaps
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                                                                           652 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG
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  Length
                           13;
Score 459; DB 23;
Pred. No. 0.00e+00;
0; Mismatches 13;
70.4%;
larity 96.2%;
Conservative
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              Best Local Similarity
Matches 513; Conser
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   Query Match
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AAS95715 568 bp mRNA EST 25-SEP-1997 1146e08.s1 NCI_CGAP_Lul Homo sapiens cDNA clone IMAGE:979910 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR AAS95715
                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 951 acd Error: 0.00 Seq primer: 940M13 fwd. from Amersham High quality sequence stop: 118. Location/Qualifiers 1.610 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 GIGGGGGCTCAGGIGGGGCCACCICIGAAGCICIGCTGACCCCIGGGCCAAGGCC-IGAC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTGCTGGT-CAGCTGCAGTCCCTGGTGGGCCGGCCACTCACTCTGGCAGNCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCACGCCAGCCATNGTTGTCCCGCCNTACTCAGTAGTTGAGTNTGGTCGCGAAGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCCAGGTGAACCACANGCTTCTCTGTGNAGC-TCCCAG-TNTTTCCAGACCAGTNNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u> AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AGACTANCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACATCACAAGCGTGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGGGGACCAAAGAAGATNGGGGGGCATGCC-AGTTCAGGGC-AGNTGCCNAGTGTAGA
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                  /db_xref="GDB:3917098"
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/lab_host="SOLR cells (kanamycin resistant)"
177 c 175 g 103 t 22 others
                                                                                                                                                                                                                                                                                                                                                                    610;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                Score 458; DB 12; L
Pred. No. 0.00e+00;
0; Mismatches 35;
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Similarity 92.3%;
527; Conservative
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ch 68.4%;
1 Similarity 95.4%;
544; Conservative
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Unpublished (1997)
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TITLE
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KEYWORDS
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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Index organism="Index organism="Organism="Index organism="Index 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente.
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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6
                                                                                                                 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrinii; Hominidae; Homo. 1 (bases 1 to 568) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GTGGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCCAAGGCCCTGAC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACCACCACCAGGGTGATGGC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 112
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Ph.D.
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                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael:
Emmert_Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
9
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Pred. No. 0.00e+00;
0; Mismatches 10; Indels
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 265.
Location/Qualifiers
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Matches 496; Conservation
                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                               Homo sapiens
g2411065
EST.
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                                                                                         ORGANISM
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AUTHORS
TITLE
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KEYWORDS
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/organism="Homo saplens"
/organism="Homo saplens"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
EcoRr: Site_2: Xhor; Cloned unidirectionally. Primer:
Oligo dT. Normal prostate epithelial call line (HPV
immortalized). 5' adaptor sequence: 5' GAATTCGGCACGAG 3'
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'
Average insert size: 1.1 kb."
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/tissue_type="spithelium" (cell line)"
/tissue_type="spithelium" (cell line)"
/lab_host="solR" (kanamycin resistant)"
31 a 179 c 181 g 97 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                    nro43068 591 bp mRNA EST 27-OCT-1997 nr95f04.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1175743 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR AA643068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 446; DB 11; Length 591;
Pred. No. 0.00e+00;
0; Mismatches 11; Indels 15; Gaps 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo. 1 (bases 1 to 591) NCI-GAP http://www.ncbi.nlm.nlh.gov/ncicgap. NCI-GAP http://www.ncbi.nlm.nlh.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Ijssue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                       472 TCGGGCACCAAAGAAGATGGGGGGCCATGCAC-GTTCTAGGGCAGCTGCCAA-TGTAGAG
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High quality sequence stop: 337.
Location/Qualifiers
1. 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                               530 GCCAAGGG-AAC-ACAGC-TTCTCTGTGAAGC 558
                                                                                                                                                                                                                                             172 GCCCAGGGGAACCACAGCCTTCTCTGTGAAGC
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162 533 222 473 281 413

US-09-047-652A-1.rst

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AA479680 541 bp mRNA EST 09-NOV-1997 2u43a07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740724 3' similar to gb:U12421_cds1 PRIPHERAL-TYPE BENZODIAZEPINE AA479680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dassa 1 to 541)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Wash T. NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTAGTTTGNCCCGCCGCCCCACTGACCAGGAGATTCACCAAGGCCCAGCCCATTTG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGGTGGTCGCGAAGGCCAG 341
went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

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2 a 160 c 164 g 104 t 6 others
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                                                                                                                                                                                                                                                                                                                                   223 ACCIGCIGGIN-AGCIGCAGICCCIGGIGGGCCGGGCACICACICIGGCAGCCGCCGICC
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                                                                                                                                                            Length 556;
                                                                                                                                                            Score 442; DB 8; Length 556 Pred. No. 0.00e+00; 0; Mismatches 11; Indels
                                                                                                                                                            67.8%;
Local Similarity 96.9%;
Les 473; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                       ACCIGCIGGIG-GACCIGCAGICCCIGGIGGGCCGGCACTCACICTGGCAGCCGC-GTCC 265
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                   CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGCGGAAGGCCAG
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      AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACATCACAAGCGTGATGGC
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RESULT

FEATURES

TITLE

COMMENT

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Query Match 65.2%;
Best Local Similarity 94.7%;
Matches 463; Conservative
                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                          92788392
EST.
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                                      Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fmail: est@wastl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 598 Std Error: 0.00

Seq primer: -41ml3 fwd. Er from Amersham

High quality sequence stop: 52.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS AA748434 541 bp mRNA EST 18-FEB-1998
DEFINITION ny0lb10.s1 NCI_CGAP_GCB1 HOMO sapiens CDNA clone IMAGE:1270459
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 0.00e+00;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
155 c 155 g 119 t 1 others
                                                                                                                                                                                                                                                                                                                                                            /clone_l1b="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                 /db_xref-"GDB:5940628"
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                                                                                                                                                                                                                                                                                                                                                                       /sex-"Female"
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1 Similarity 97.98;
461; Conservative
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clond distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);; mRNA sequence. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), 50 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 109 110 GTGGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCCAAGGCCCTGAC 169 Homo sapiens Eukaryotes, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo. 1 (bases 1 to 541) 170 AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACCATCACAAGCGTGATGGC 229 ñ Length 541; 3 others Score 425; DB 15; Length 54 Pred. No. 0.00e+00; 0; Mismatches 23; Indels /db_xref='taxon:9606"
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/tissue_type="germinal center B cell"
/lab_host="DH108" Insert Length: 874 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 358. Location/Qualifiers 541
 /organism="Homo sapiens"

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US-09-047-652A-1.rst

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human.
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similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HVPAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 506)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,Y., Willenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wille,T., Waterston,R. and Wilson,R.
WashD-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 443.
472 ACCTGCTGCTGCAGCTGCAGTCCCTGGTGGGCCGGGCACTCTGGCAGCCGCCGTCC 413
                                                                        CGGTAGGTGNNCCGGCCCCCCACTGACCAGCAGGAGATTCACCAAGGCCCCAGCCATTT 468
                                                                                                                                                                         289 CCCACGCCAGCCAIGGIIGICCCGCCAIACGCAGIAGIIGAGIGIGGICGCGAAGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/organism="Homo sapiens"
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SOURCE
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AA036726 551 bp mRNA EST 10-MAY-1997 zk30b07.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 472021 3' similar to gb:012421_cdsl PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
AA036726 g1509983
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkln,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                          274 CCCATGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGCGAAGGCCAG
                                                                                                                                                                                                                                              94 GTGGGGGCTCAGGTGGGGCAACCTCTGAAGCTCTGCTGACCCCTGGGGCCAAGGCCCTGAC
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                                                                                                                                               Length 506;
                                                                                    1 others
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                                                                                                                                           Score 424; DB 7; Le
Pred. No. 0.00e+00;
0; Mismatches 10;
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pregnant uterus"
/lab_host="bH10B"
complement(<1...>506)
/db_xref="GDB:6044096"
a 150 c 158 g 8
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                                                                                                                                       / Match 65.0%;
Local Similarity 96.9%;
nes 463; Conservative
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                                                                                                                                                   double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library contructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                Score 414; DB 5; Length 551;
Pred. No. 0.00e+00;
0; Mismatches 24; Indels 10; Gaps 10;
                                                                                              IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 695 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 321.
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                                                                                   /organism-"Homo sapiens"
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/db_xref="GDB:3758023"
                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
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Best Local Similarity 93.5%;
Matches 491; Conservative
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AA838533 505 bp mRNA EST 18-MAR-1998
es99all.12 NOI_CGAR_PR25 Homo sapiens cDNA clone IMAGE:1410908
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.

LOCUS DEFINITION

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CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                             Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright, Ph.D.
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                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
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/clone_lib="NCI_CGAP_Pr25"
/tissue_type="epithelium (cell line)"
/lab_host="SOLR (kanamycin resistant)"
148 c 156 9 89 t
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High quality sequence stop: 323.
Location/Qualifiers
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 62.1%;
1 Similarity 94.9%;
444; Conservative
                                                                                                                                                                                  Unpublished (1997)
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                                                                                                              EST 19-FEB-1998 BABGO1.s1 NCI_CGAP_GCBI Homo sapiens cDNA clone IMAGE:1338240 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR AMB05072
                                                                                                                                                                                                                                              Eukaryotae, Metazoa, Chordata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 543)

NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Score 399; DB 15; Length 543;
Pred. No. 0.00e+00;
0; Mismatches 22; Indels 7;
                                                                  232 TCGGGCACCAAAGAAGATGGGGGGCCATGCCCAGTTCAGGGCCAGCTG 185
                                                    458 TCGGCCACCAAAGAAGGATGGGGGGCATGGCAAGTTCAGGGGCCAGCTG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 903 Std Error: 0.00
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High quality sequence stop: 272.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 61.2%;
1 Similarity 94.1%;
463; Conservative
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Gaps

54 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 113

Matches

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AA768741 507 bp mRNA EST 08-FEB-1998 ob22901.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1334464 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN); mRNA sequence.

AA768741
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Frimates; Catarrhini; Hominidae; Homo.

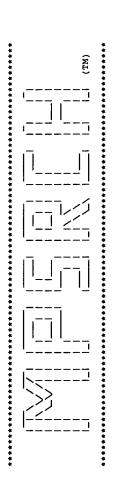
1 (bases 1 to 507)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                   GTGGGGGGTCAGGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCCAAGGCCTCGAC
                                                  174 AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACATCACAAGCGTGATGGC
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Insert Length: 612 Std Error: 0.00
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High quality sequence stop: 484.
Location/Qualiflers
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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab.host="bH10b"
a 144 c 151 g 101 t
                                                            5,
                                              ch 60.4%; Score 394; DB 13; Length 507; 1. Similarity 96.5%; Pred. No. 0.00e+00; 435; Conservative 0; Mismatches 11; Indels 9
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Search completed: Tue Jul 21 15:24:46 1998 Job time: 776 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

MasPar time 108.16 Seconds 767.738 Million cell updates/sec Tue Jul 21 16:05:14 1998; Run on:

Fabular output not generated.

Title:

1 CCACGGCGAGGGTCTCCGCT........GTTCTTGGAACATGGAATTT 652 GGTGCCGCTCCCAGAGGCGA........CAAGAACCTTGTACATAAA >US-09-047-652A-2 (1-652) from US09047652A.seq 652 Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

176886 segs, 63680241 bases x Dbase 0; Query 0 •• STD Searched: Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq31-2 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 10:part16 20:part20 21:part21 22:part22 23:part23 24:part24 22:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 33:part35 36:part36 37:part37

Mean 8.516; Variance 5.456; scale 1.561 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Res	Result No.	Score	Query	ouery Match Length DB	DB	1D	Description	Pred. No.
:	-	238	36.5	272	2	T22195	Human gene signature	6.34e-134
U	7	44	6.7	91	σ	051746	Oligonucleotide probe	2.41e-11
υ	m	41	6.3	204	Н	N81164	Base substituted E.co	1.11e-09
	4	40	6.1	91	σ	051746	Oligonucleotide probe	3.92e-09
U	'n	36	5.5	114	12	070465	Generic DNA sequence	5.68e-07
	φ	36	5.5	204	Н	N81164	Base substituted E.co	5.68e-07
	7	35	5.4	114	12	070469	Generic DNA sequence	1.93e-06
	ω	34	5.2	114	12	070468	Generic DNA sequence	6.48e-06
	σ	34	5.2	114	12	070472	Generic DNA sequence	6.48e-06
	9	34	5.2	114	12	070465	Generic DNA sequence	6.48e-06
	11	34	5.2	114	12	970467	Generic DNA sequence	6.48e-06
υ	13	34	5.2	114	17	970468	Generic DNA sequence	6.48e-06
υ	13	34	5.2	114	17	070467	Generic DNA sequence	6.48e-06
U	14	33	5.1	114	7	070469	Generic DNA sequence	2.16e-05

7 100-05	7.10e-05	7.10e-05	7.10e-05	2.31e-04	2.31e-04	7.44e-04	7.446-04	7.446-04	2.36e-03	2.36e-03	2.36e-03	7.41e-03	7.41e-03	2.29e-02	2.29e-02	2.29e-02	2.29e-02	6.95e-02	6.95e-02	6.95e-02	6.95e-02	2.08e-01		2.08e-01	2.08e-01	•	•	ヿ	- 0	6.10e-01
Gonorico DNA concor	DNA	doth		Generic DNA sequence	Human interleukin 8 a	Generic DNA sequence	Generic DNA sequence	Chymase antisense oli	Generic DNA sequence	Generic DNA sequence	Human MDNCF antisense	Generic DNA sequence	Human IL6 antisense o	Generic DNA sequence	Human endothelin ETA	Human interleukin 8 a	HCV envelope region n	Human IL5 antisense o	96	Chymase antisense oli	Inducible nitric oxid	Human RANTES antisens	Human MDNCF antisense	Substance P antisense	Substance P antisense	ar	ပ္ပ	Human defensin 1 anti	Human cathepsin G ant	ept
070466	070470	T76405	T76405	070470	T76363	070473	070466	T76452	970471	070473	T76270	970471	T76233	070472	T76423	T76363	935072	T76219	T76233	T76452	T76527	T76307	T76270	T76438	T76438	T13610	T76152	in	T76290	10
5	12	31	31	12	32	12	12	31	12	12	31	12	31	12	31	32	ø	31	31	31	31	31	31	31	31	21	31	31	31	33
114		178			172	114	114	190	114	114	168	114	128	114	125	172	565	8	128	190	379	162	168	250	250	82	130	÷	161	264
0	. 0	6.	4.9	4.8	4.8	4.6	4.6	4.6	4.4	4.4	4.4	4.3	4.3	4.1	4.1	4.1	4 . 1	4.0	4.0	4.0	4.0	3.8	3.8	3.8	3.8	3.7	3.7	3.7	3.7	3.7
33	3 6	32	32	31	31	30	30	30	53	5	5	58	58	27	27	27	27	56	56	56	56	22	52	22	25	77	24	24	24	24
<u>.</u>	0 16	-	c 18	19	20	21	c 55	23	7	c 25		27	28		30	c 31	32	33	e	c 35	m	37	ი 38	39	c 40	41	42	43	44	45

#### ALIGNMENTS

double-stranded DNA, or its complementary strand or the corresp.

double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-turranslated sequence; sunique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 272 BP; 48; 78; 86 G; 51 T; Gene signaturė; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss. Matsubara K, Okubo K;
WPI: 95-206931/27.
Tdentfying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human T T22195 standard; cDNA to mRNA; 272 BP. Claim 1; Page 1068; 2245pp; Japanese. 27-AUG-1996 (first entry) Human gene signature HUMGS03766. 11-NOV-1994; J01916. 12-NOV-1993; JP-355504. (MATS/) MATSUBARA K. (OKUB/) OKUBO K. tissues RESULT 

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               samples
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                                                                                       254 GATCTCCTGCTGGTCAGTGGGGGGGGGGGAGCCACTACCGTGGCCTGGTACCAGGTGAGC 313
                                               1 gatctcctgctggtcagtggggggggggggagc-actaccgtggcctggtaccaggtgagc 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                            Gaps
                                                                                                                              aactactgcgtatggcgggacaaccatggctgcatgggggacggcggctgccagagtga
                                                                                                                                                                     gtgcccggcccaccagggantgnagntgnaccagnaggtgccatnangtttntaatntag
                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (051735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59. 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N81164 standard; DNA; 204 BP.
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; ss.
Escherichia coli.
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                                                                                                                                                                                                                                                                                      31-WAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                            Synthetic.
EP-571911-A.
01-DEC-1993; 108325.
24-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD. Spears PA;
New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria acid in
       Length 272;
       Score 238; DB 20; Length 27
Pred. No. 6.34e-134;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 9; Length 91;
Pred. No. 2.41e-11;
46; Mismatches 4; Indels
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/*tag- a
//uction-multiple cloning site
187..204
                                                                                                                                                                                                                       494 TGGCCGTCACGCTTTCATGACCACTGGGCCTG 525
                                                                                                                                                                                                           240 tggccgtnangttttaatgaccantgggnctg 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                        .r 2
O51746 standard; cDNA; 91 BP.
O51746;
       36.5%;
llarity 92.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match
Local Similarity 3.8%;
les 2; Conservative
                Local Similarity
nes 251; Conser
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        Query Match
Best Local 5
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                           Matches
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DD 08
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Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be maplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which cocurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 ymrttthhyrrmrbnvyrdyn-rsdaaawyccyrrsvkydccynachhddhyvybbbvyn 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 CAGCTGCCCCAGTGTAGAGGCCCAGGGGAACCACAGCCTTCTCTGTGAAGCCTCCCAGCTC 131
                                                                                                                                                                                                                                         Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                 (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ssvhsyyvvhvvshhhsvhhvvhhvhvsvvvhh-vvhvvhhvhyhvyvsvct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 204;
Pred. No. 1.11e-09;
60; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 vhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T
Q51746 standard; cDNA; 91 BP.
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24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.3%;
Best Local Similarity 7.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 A;
                                                                                                                        US-034819.
/*tag-
                                                            05-MAY-1988.
30-MAR-1988; 105163.
                                                                                                                                                                                                          WPI; 88-279927/40.
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                                                                                                                        03-APR-1987;
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EP-571911-A.
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Escherichia coli.
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PR 101-FEB-1993; US-01316.

PR 30-DEC-1993; US-01316.

Probles DM, KAY BK;

WHOT'S DM, WHOT'S D
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               O70465 standard; DNA; 114 BP.
070465 standard; DNA; 114 BP.
070465 standard; DNA; 114 BP.
0504APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; effectiv rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 banbanbanbanbubtgcanbanbanbanbanbanbanbanbanbanbanban
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N8 NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
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Pred. No. 5.68e-07;
33; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
comments)"
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5.68e-07;
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Similarity 4.5%;
5; Conservative
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Best Local Similarity
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93 hyrrmrbnvyrdyn-rsdaaawyccyrrsvkydccynachhddhyv-ybbbvynvhnhnn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                (SUSO) SUOMEN SOKERI OY.
Lebtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen T;
WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
Introducing random point mutations into more a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 CIGGIACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGGCCCTGT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suiteble host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bischosure; page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 Others;
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//tote= 'this sequence represents '2'; 2 can be
sequence of 6,9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 204;
Pred. No. 5.68e-07;
53; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 cncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvchccgatc 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGGCACGCTTACTCAGCCATGGGGTACGGCTCCTACCTGGTC 124
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                                                                                  /*tag= a
/function=multiple cloning site
187..204
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
55..60
/*tag= a
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Location/Qualiflers
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1D 070469; atandard; DNA; 114 BP.

AC 070469; DT 07-APR-1995 (first entry)
DE Generic DNA sequence to generate to generate to generic DNA sequence to generate to a finit we fector domain; concatenated to direct; rapid; detection; screed to synthetic.

FT Actor is a first of the first of the first of the key for the first of the fir
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Best Local Similarity 15.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           US-034819.
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                                         misc_feature
                                                                                                                                                                         primer_bind
                                                                                                                                                                                                                                                                                                             05-MAY-1988
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CC (700469 is a generic DNA sequence used to generate random TSAR peptide
This generic formula can be represented as follows: X(TGC)(NNB)10-
CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
CC sequence generates peptides that are cloverleaf in structure. Other
CG generic sequences are shown in 070465-68. Other specific peptides
CG generic sequences are shown in 070465-68. Other specific peptides
CG generated by these generic sequences are shown in R65150-54. TSARS are
CG concatenated heterofunctional proteins or peptides, comprising at least
CG a second effector peptide portion that is chemically or biologically
CA active. They may further comprise a linker peptide between the 2 domains.
CG ontains 2 or 4 cysteine residues positioned in, or flanking, the
CG contains 2 or 4 cysteine residues positioned in, or flanking, the
CG contains 2 or 4 cysteine residues positioned in, or flanking, the
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Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)62(NNB)7(TGC)(NNB)10Y. X and X are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding doma
effector domain; concateneated heterofunctional protein; inker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 bnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnptg 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GECTGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCCTACCTGGTCTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 12; Length 114;
Pred. No. 1.93e-06;
31; Mismatches 73; Indels
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G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection in a screening process. Sequence 114 BP; 0 A; 4 C
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31-JAN-1994; US-189331.
(UNIC-) UNIV NORTH CAROLINA.
EQWIKES DM, RAY BK;
WPI; 94-279739/34.
P-PSDB; R65154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 8
Q70468 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%;
Similarity 6.3%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radiosotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tersule, Noove, to peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comparising a binding domain and an effector domain comparising a bisclosure; Page 36; 255pp; English.

20 70472 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)1(CAC)(NNB)1(CAC)(NNB)(CAC)(NNB)2(AND)6 (CAC)(NNB)4.X and Y are flanking restriction sites of x is not the same as Y) that are not specified further. The peptides generated by this and other generic sequences: (970470.73) have invariant histidine residues incorporated into variant sequences. TSARs at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically cative molety, eg. metal two to deliver a chemically or biologically active molety, eg. metal con, radiolsotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg.
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R65151-54. TSARs are concatenated heterofunctional proteins or peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070472;
10-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 6.48e-06;
34; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 12;
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/note= "encoded by Z"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-12-131-JAN-1994; US-189551.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q70472 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                            5.2%;
Similarity 2.7%;
3; Conservative
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US-176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9418318-A
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3.68;

Best Local Similarity

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PF 01-FEB-1993; US-01316.

PR 101-FEB-1993; US-01316.

PR 30-DEC-1993; US-01316.

PR (UNIV.) UNIV NORTH CARDLINA.

POWAREA DM, KAY BK;

WHO: 94-27939/44.

PP 55DB; R65150 and R65151.

PP FSDB; R65150 and R65181.

Comprising a binding domain and an effector domain

CC R65181-54. TSARS are concatenated by these generic sequences are shown in CC R65181-54. TSARS are concatenated by these generic sequences are shown in CC R65181-54. TSARS are concatenated beterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptides are also designed so confers some degree of conformational rigidity to the peptides. The other concatenated contains 2 or 4 cysteine residues positioned in, or I lanking, the unpredicted or variant residues. These residues confers concerned sequences or conformational rigidity to the peptides. The TSARS confers some degree of conformational rigidity to the peptides. The TSARS confers some degree of conformational rigidity to the peptides. The CC rempress peptide, toxin or enzyme, to the specific target or on the concount or polyclonal antibodies and therefore circumvent the need conformational artipodes and therefore circumvent the need conformation The TSARS are easily characterised and have designed cativity allowing direct and rapid detection in a screening process.

Sequence 114 BB; CASARS are easily characterised and have designed cativity allowing direct and arginal and a replace of the detection in a screening process.
                                                                                                                                                                                    ö
monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 6 A; 12 C; 0 G; 0 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                070465 standard; DNA; 114 BP.
070465;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                           3 bcacnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbcacnnbcacnnbnnbnnbnnnnnn 62
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                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                    63 bnnbnnbnnbnnbnnbcaconnbnnbnnbnnbcaccacnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                            73 CCCTGTCTGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCCTACCTGGTC 124
                                                                                                                                       Length 114;
                                                                                                                                  Score 34; DB 12; Length 114
Pred. No. 6.48e-06;
29; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55..60
/*tag= a
/note= "this sequence represents 'Z'; Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of 6, 9 or 12 nucleotides (see comments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                       5.28;
                                                                                                                                                                                 Conservative
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                                                                                                                                                          Best Local Similarity
Matches 12; Conser
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01-FEB-1994; U
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

C70467 is a generic DNA sequence used to generate random TSAR (Totally

C8 Synthetic Affility Reagents) peptides. This generic formula can also be

represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)17. X

and Y are flanking restriction sites (X is not the same as Y) that are

C8 on the specified further. Other generic sequences are shown in R65151-34. TGARS are concatenated by these generic sequences are shown in

C85151-34. TGARS are concatenated beterofunctional proteins or peptides,

C97 comprising at least two functional regions - a binding domain with

Affinity for a ligand and a second effector peptide portion that is

C98 comprising at least two functional regions - a binding domain with

Affinity for a ligand and a second effector peptide portion that is

C98 comprising at least two functional regions - a binding domain with

Affinity for a ligand and a second effector peptide portion that is

C99 comprising a TGAR binding domain can be used in vivo to

C90 comprising a TGAR binding domain can be used in vivo to

C91. They can also replace the function of macromolecules, eg.

C91. They can also replace the function of macromolecules, eg.

C91. They can also replace the function of macromolecules, eg.

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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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/note= *this sequence represents '2'; 2 can
sequence of 6, 9 or 12 nucleotides (see
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Pred. No. 6.48e-06;
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Pred. No. 6.48e-06;
33; Mismatches 75;
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Q70467 standard; DNA; 114 BP
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(UVNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
WPI; 94-279739/34.
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llarity 3.6%;
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30-DEC-1993;
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Length 114;

DB 12;

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5.2%;

Query Match

Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.

05-APR-1995 (first entry)

070467

Location/Qualifiers

55..60

misc_feature

Synthetic.

can be a

/*tag= a
//note= "this sequence represents '2'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)."

(UYNC-) UNIV NORTH CAROLINA.

Fowlkes DM, Kay BK; WPI; 94-279739/34.

P-PSDB; R65153

US-189331

31-JAN-1994;

US-013416. US-176500.

U00977

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PT Forbials Robinson Street, which bind a ligand - by screening a recombinant vector library expressing fusion proteins accombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by screening a binding domain and an effector domain bisclosure; Page 35; 255pp; English sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be compared as follows: X(NNB)1(TGC)(NNB)7(TGC)(NNB)10x. X and X are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in O70466-68. Comparising at least two functional regions - a binding domain with comparising at least two functional regions - a binding domain with a comparising at least two functional regions - a binding domain with chemically or biologically active. They may further compities a linker peptide between the 2 domains. The oilgonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rigidity to the peptides. The TSARs or compers. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active modety, eq. metal ion, radiosotope, peptide, toxin or enzyme, to the specific target or on the contional or polyclonal antibodies and therefore circumvent the need monoclonal or polyclonal antibodies and accomplex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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sequence of 6, 9 or 12 nucleotides (see
comments)"
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33; Mismatches 75; Indels
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Fowlkes DM, Kay BK;
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Similarity 3.6%;
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30-DEC-1993; US-176500.
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WPI; 94-279739/34.
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01-FEB-1994;
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Territy Montains or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by screening a recombination of bisclosure; Page 35; 255pp; English.

COMPACT is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(NNB)12(N
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Pred. No. 6.48e-06;
34; Mismatches 75; Indels
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RESULT 13 ID Q70467 standard; DNA; 114

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O5-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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PF 01-FEB-1994; U00977.

PR 01-FEB-1994; US-013416.

PR 10-PEB-1995; US-013416.

PR 10-PEB-1995; US-013630.

PR 11-AN-1995; US-013630.

PR 17-AN-1995; US-013630.

PR 17-AN-1996; US-01
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Search completed: Tue Jul 21 16:07:07 1998 Job time: 113 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 36.85 Seconds 949.152 Million cell updates/sec Tue Jul 21 16:07:26 1998; Run on:

Tabular output not generated.

>US-09-047-652A-2 (1-652) from US09047652A.seq 652 Description: Perfect Score: N.A. Sequence:

1 CCACGGCGAGGGTCTCCGCT.......GTTCTTGGAACATGGAATTT 652 GGTGCCGCTCCCAGAGGCGA........CAAGAACCTTGTACCTTAAA

Scoring table:

TABLE default Gap 6

Dbase 0; Query 0 STD Nmatch 104157 seqs, 26825796 bases x

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 8.110; Variance 4.794; scale 1.692 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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#### ALIGNMENTS

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Sequence 14, Application US/08232463
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ZIB 2313-0299
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE ROAD NATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
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NAME: BREWY, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 39,7114 IMMU
TELECOMBUNICATION NUMBER: 29,768
REFERENCE/COCKET NUMBER: 39,7114 IMMU
TELECOMBUNICATION NUMBER: 29,768
REFERENCE/COCKET NUMBER: 39,7114 IMMU
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Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: DOWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
                                                                                                                                                                                                                                                                                                                                      Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGT 185
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                                                                                                                                                                                                                                                                                                                                                                  7 SSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANY 66
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: Sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                        Length 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIF: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      Score 36; DB 1; I
Pred. No. 1.55e-08;
82; Mismatches 98
                                  2307E-540
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US-08-238-163-5 STANDARD; DNA; UNC; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/238,163 FILING DATE: 03-MAX-1994 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 KSNVSNNCGGGNKRDVSSYANNKCCGSSC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 GCGGCCAGCGGCTCACCTGGTACCAGGC 296
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYRE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                     f match 5.5%;
Local Similarity 13.4%;
les 28; Conservative
                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: LABAVITCH, John M.
APPLICANT: LABAVITCH, John M.
APPLICANT: TOWELL, Ann
APPLICANT: TOWELL, Ann
APPLICANT: POWELL, Ann
APPLICANT: SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                     ö
                                                                                                                                                                                 133 GCTGGGAGGCTTCACAGAAGGCTGTGGTTCCCCTGGGCCTCTACACTGGGCAGCTGGC 192
                                                                                                                                                                                                                                                               CCTGTCTGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCCTACCTGGTCTGGAAAGA 132
                                                                                                                                                                                                                                                                                                                                                                                   193 CCTGAACTGGCCATGGCCCCCCATCTTTGGTGCCCGACAAATGGGCTGGGCTTGGT 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 TCTCCGCTGGTACGCCGGCCTGCAGAAGCCCTCGTGGCACCCGCCCCACTGGGTGCTGGG 72
                                                                                                                                                       Gaps
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                                                                            CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                      6.0%; Score 39; DB 1; Length 7218; Similarity 0.3%; Pred. No. 2.64e-10; 1; Conservative 203; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 2
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
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FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/Me---
JURPEN: PATAMARE: PATAMARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08238163 Sequence 5, Application US/08238163 Patent No. 5569830 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
 LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                           TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1427 YYYYYYYG 1435
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                                                                                                                                                     Matches
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                             3.8%;
Best Local Similarity 9.9%;
Matches 7; Conservative
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                                                                                       LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 9.9%;
Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                            128 TSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKS 187
                                                                                                                                                                                                                                                                                                                                                                                        9 SSVVSRTASCNDKAKKDGNTISSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNY 68
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICART: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                               Score 35; DB 1; Length 215;
Pred. No. 5.93e-08;
81; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 4
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                       2307E-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMBER: PCT/US95/11934
20-SEP-1995
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REPERBUE/DOCKET NUMBER: 2307E-
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 543-9600
TELEFAN: (415) 543-9603
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TWPE: nucleic acid
TWPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                    188 NVSNNCGGGNKRDVSSYANNKC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                        484 TGTGATGTGGTGGCCGTCACGC 505
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                                                                                                                                                                                                                                               Query Match 5.4%;
Best Local Similarity 12.4%;
Matches 25; Conservative
                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20
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                                                                                                                                                                                  Gaps
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Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICART: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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Pred. No. 2.03e-02;
20; Mismatches 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 2; Length 81;
Pred. No. 2.03e-02;
20; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPAtible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
NAME: MISTOCK, S. Leelle
REGISTRATION NUMBER: 11,01-196-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: LISS Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                      .T 5
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
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            0; Gaps
                                                                                                                                         APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score.24; DB 2; Length 74; Similarity 7.7%; Pred. No. 6.68e-02; 5; Conservative 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934 FILING DATE: 20-SEP-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
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PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
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PCT-US95-11934-100 STANDARD; DNA; UNC; 74
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                                                                                                               Sequence 94, Application PC/TUS9511934 Sequence 94, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                              ZIP: 10036
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
TELEX. (212) 869-9741/8864
TELEX: 6614 PENNE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: streambeness: single
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                      CITY: New York
STATE: New York
                                                492 GGTGGCCGTCA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                   70 BNNBNACGCCA 80
                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 GGCCA 294
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ID PC
AC XX
DT SK
CC SK
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Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                    Aniigen Binding Peptides (Abtides) From
Peptide Libraries
103
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                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATCORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 1101-196-228
REGISTRATION NUMBER: 1101-196-228
TELEFANCE/DOCKET NUMBER: 1101-196-228
TELEFANCE/DOCKET NUMBER: 1101-196-228
TELEFANCE (212) 799-9090
TELEFANCE (212) 799-901
TELEFANCE (212) 799-901
TELEFANCE (212) 69-9741/8864
TELER: (212) 869-9741/8864
TELER: 74 base pairs
TYPE: nucleic acid
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
TITLE OF INVENTION: Antigen Binding Perile OF INVENTION: Antigen Binding Perile OF INVENTION: Apptide Libraries NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 л
РСТ-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           USA
      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 ACCACA 489
                                                                                                                                                                                                                                                                                                                                  STATE: Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ACCACA 78
                                                                                                                                                    298 GGCCA 294
                                                                                                                                76 CGCCA 80
                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                                                                                                                 Gaps
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Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICATY: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
TITLE OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE:
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                           Score 24; DB 2; Length 75;
Pred. No. 6.68e-02;
20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTE: Floppy disk
COMPUTE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/ACE:...
                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                           T 9
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. LEGELLE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECHOMNICATION:
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                      1101-196-228
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MISTORK, S. Leslie
REGISTRATION NUMBER: 1101-196-228
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELERAX: (212) 780-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                            Query Match
Best Local Similarity 6.2%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                      : : |
492 GGTGG 496
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                                                                                                  0; Gaps
                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICART: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 2; Length 81;
Pred. No. 6.68e-02;
19; Mismatches 41; Indels
Score 24; DB 2; Length 81;
Pred. No. 6.68e-02;
20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTOREX/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET UNMBER: 1101-196-228
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET UNMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9091
TELEFAX: (212) 669-9741/8864
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRNDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                           JT 10
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7%;
Similarity 9.1%;
6; Conservative
Query Match 3.7%;
Best Local Similarity 7.7%;
Matches 5; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                        Sequence 97, Application PC/TUS9511934
Sequence 97, Application PC/TUS9511934
Sequence 97, Application PC/TUS9511934
GENERAL InvoRMATION:
CTITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPER: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144, Application US/08471052A
Sequence 144, Application US/08471052A
Sequence 144, Application US/08471052A
Patent No. 5625031
GENERAL INFORMATION:
APPLICANT: Ray, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCES: 166
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 2; Length 82;
Pred. No. 6.68e-02;
19; Mismatches 43; Indels
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         ATTONNEL TREVERATION:

NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELESTA: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP: 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .r. 12
US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
                      T 11
PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.7%;
Best Local Similarity 10.1%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 GGGTACGG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 BNNBNNBGG 75
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135 AGCTCTTTCCAGACCAGGTAGGAGCCGTACCCCATGGCTGAGTAGAGCGTGCCCCAGACA 76
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Sequence 143, Application US/08471052A
Sequence 143, Application US/08471052A
CGENERAL INFORMATION:
CGENERAL INFORMATION:
CTITLE OF INVENTION:
TOTALL OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CORRESPONDENCE:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COMPUTER READABLE FORM:
COMPUTER:
COMPU
STREG...
CITY: New YOLK
STATE: New YOLK
STATE: New YOLK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
TING DATE: 06-UUNE-1995
TING DATE: 06-UUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 1; Length 66;
Pred. No. 2.15e-01;
18; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .т. 13
US-08-471-052A-143 STANDARD; DNA; UNC; 68 ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATORNEZ-YAGENT INRORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELEPHONE: 212 869-8864/9741
TELEFAX: 212 869-8864/9741
TELEFAX: 6641 PENNIE
INFORMATION: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH. 66 bases
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RESULT
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Sequence 142, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOWLKES, D. M.
APPLICANT: FOWLKES, D. M.
APPLICANT: POWLKES, D. M.
APPLICANT: POWLKES, D. M.
APPLICANT: POWLKES, D. M.
APPLICANT: POWLKES, D. M.
STREE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSED: ADDRESSED:
                                                                                                                                                                                                                                                                                                                             Query Match 3.5%; Score 23; DB 1; Length 68; Best Local Similarity 13.4%; Pred. No. 2.15e-01; Matches 9; Conservative 18; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER KEDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGBNT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION WUMBER: 18,372
FEGISTRATION NUMBER: 18,372
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869 8864/9741
TELEFAX: 212 869 8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 68 BP; 3 A; 3 C; 5 G; 3 T; 54 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. 14
US-08-471-052A-142 STANDARD; DNA; UNC; 69 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101-179
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TELECOMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELERA: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
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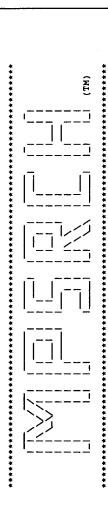
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                                                                                                                              468 GETGGTGCAGCTGCAGTCCCTGGTGGGCCGGGCACTCACTCTGGCAGCCGCCGTCCCCCA 409
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C Sequence 100, Application PC/TUS9511934
C GENERAL INFORMATION:
C APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
C TITLE OF INVENTION: Peptide Libraries
C NUMBER OF SEQUENCES: 103
C CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
C STREE: 1155 Avenue of the Americas
C CITY: New York
C COUNTRY: USA
  Score 23; DB 1; Length 69;
Pred. No. 2.15e-01;
17; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 2; Length 74;
Pred. No. 2.15e-01;
19; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPERATION
COPERATION SYSTEM: PC-005/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NORMER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NORMER: 18,872
REGISTRATION NUMBER: 1101-196-228
REGISTRATION NUMBER: 1101-196-228
TELEPHONE: (212) 799-9090
TELEPHONE: (212) 799-9010
TELEFAX: (212) 799-9741/8864
TELEX: (614) PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  .T 15
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Tue Jul 21 16:08:07 1998
Query Match
Best Local Similarity 13.6%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.5%;
Best Local Similarity 9.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 NNACCAC 70
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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 760.56 Seconds 1145.078 Million cell updates/sec Tue Jul 21 15:51:59 1998; Run on:

Tabular output not generated.

>US-09-047-652A-2 (1-652) from US09047652A.seq 652 Title:

1 CCACGGCGAGGTCTCCGCT.......GTTCTTGGAACATGGAATTT 652 GGTGCCGCTCCCAGAGGCGA.......CAAGAACCTTGTACCTTAAA Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 •• STD Nmatch

1759237 seqs, 667866413 bases Searched:

×

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est54 Database:

1:em_estl 2:em_est3 genbank-estl06 Database:

3:9b_est1 4:9b_est10 5:9b_est11 6:9b_est12 7:9b_est13 8:9b_est14 9:9b_est15 10:9b_est16 11:9b_est17 12:9b_est18 13:9b_est19 14:9b_est2 15:9b_est20 16:9b_est2 17:9b_est2 17:9b_est2 18:9b_est4 20:9b_est5 21:9b_est6 22:9b_est7 23:9b_est8 24:9b_est9 25:9b_gss 26:9b_sts

Mean 10.451; Variance 2.423; scale 4.313 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	888888888888	0.00e+00 0.00e+00
Description	0,20,0,0,2220,20	zk30b07.sl Soares preg oe39all.sl NCI_CGAP_Pr
£ £	AA724486 AA715735 AA715735 AA161033 AA069473 AA695715 AA643068 AA210894 AA776880 AA74880 AA74880	AA036726 AA838533
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Score	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	414
ult No.	110087004321	13
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Emmert-Buck, M.D., Ph.D.
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AA587126 g2397940
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I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-733399. Subtraction by Soares and M. Fatima Bonaldo."

/clone="1327269"
/clone="1327269"
/clone="115-"Scares NFL T GBC SI"
/lab.host="10H10B"
166 c 166 g 91 t 3 others
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
                                                                                                                      Score 498; DB 15; Length 54
Pred. No. 0.00e+00;
0; Mismatches 8; Indels
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| Similarity 98.4%;
| 503; Conservative
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CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/lab_host="SolR (kanamycin resistant)"
<1. .>572 173 g 96 t
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 
                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryotae; Matazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarzhini; Hominidae; Homo.

1 (bases 1 to 567)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Krizman, D., Rucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theislang, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Unpublished (1997)
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Pred. No. 0.00e+00;
0; Mismatches 12; Indels
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167 c 175 g 98 t 1 others
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/clone="378559"
/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
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WashUrwer for the following washUrwers and washUrwers washIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu Email: estewatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoelmage.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 425.

High quality sequence stop: 425.

I. 563

I. 563

// Arran Homo saplens*
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4A161033
g1735356
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CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTGTGGTGGAAGGCCAG 328
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AAG69479
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WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should is the in mind should you use this clone.
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Primates; Catarrhini; Hominidae; Homo.
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1 (bases) Larkins, nominitate; nomin.

1111er,L., clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.

Parsons,J., Rifkln,L., Rohlfing,T., Tan,F., Trevaskis,E.,

Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

Unpublished (1995)
                                                                                                                                                                                                                                                                              ACCTGCTGGTN-AGCTGCAGTCCCTGGTGGGCCGGGCACTCACTCTGGCAGCCGCCGTCC
                                                   AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG
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0; Mismatches 13; Indels
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AA595715 568 bp mRNA EST 25-SEP-1997 n146e08.s1 NCI_CGAP_Lul Homo sapiens CDNA clone IMAGE:979910 amiliar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN); mRNA sequence.
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6
                                                                                                                                                                                                                                                                                                           Length 610;
This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for fu Insert Length: 951 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 118.
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Pred. No. 0.00e+00;
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Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
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9
                                                     Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo.

1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NALJOBAI Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.3%; Score 452; DB 10; Length 568; Best Local Similarity 96.9%; Pred. No. 0.00e+00; Matches 496; Conservative 0; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                      cDNA Library Arraying: Greg Lennon, Ph.D.
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 265.
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nr95f04.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1175743
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.
AA643068
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 446; DB 11; Length 591;
Pred. No. 0.00e+00;
0; Mismatches 11; Indels 15; Gaps 15;
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Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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1111 | 111 | 111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
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High quality sequence stop: 337.
Location/Qualifiers
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/organism="Homo sapiens"
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AA479680 541 bp mRNA EST 09-NOV-1997 2u43a07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740724 3. similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Eukaryotae; Metarrhini; Hominidae; Homo.

1 (bases 1 to 541)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="IMAGE:683002"
/clone=!lb="Worl_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
complement(<1. .>556)
/db_xref="GDB:5586322"
/db_xref="GDB:5586322"
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Pred. No. 0.00e+00;
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Similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN); mRNA sequence.

AA210894
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                               266 CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGCGAAGGCCAG
         AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACCACATCACAAGCGTGATGGC
                                                                   208 ACCIGCIGGIG-AGCIGCAGICCCIGGIGGGCCGGCCACTCIGGCAGCCGC-GICC
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Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                               Fax: 20 watton, wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (inf@@image.llnl.gov) for further information.
Insert Length: 598 Std Error: 0.00
Seq primer: -44ml3 fwd. ET from Amersham
High quality sequence stop: 52.
Location/Qualifiers
1. 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS AA748434 541 bp mRNA EST 18-FEB-1998
DEFINITION ny0lb10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 CGGTAGTGGCNGC-GCCGCCCCACTGACCAGCAGAGATCCACCAAGGCCCAGCCCATTT 491
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
155 c 155 g 119 t 1 others
                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares ovary tumor NbHOT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 437; DB 11;
Pred. No. 0.00e+00;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                           /clone="740724
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.9%;
Matches 461; Conservative
                           Tel: 314 286 1800
Fax: 314 286 1810
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Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-blo.llnl.gov/bbrp/image/image.html
similar to gb:U12421_cdsl PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
AA748434
                                                                                                                                                                          Eukaryotae: Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrini, Hominidae; Homo. 1 (bases 1 to 541) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 109
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/clone="IMAGE:1270459"
/clone=lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
152 c 166 g 100 t 3 oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 874 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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533 213 473 413 333

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AA036726 551 bp mRNA EST 10-MAY-1997 zk30b07.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 472021 3' similar to gb:012421_cdsl PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
AA036726 g1509983
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 GIGGGGGCTCAGGIGGGGCAACCICIGAAGCICIGCIGACCCCIGGGCCAAGGCCCIGAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGCCAGGTAGGGGTAGAGCAGGCGGGCGAGCGGGCTCACCTGGTACCAGGCCAC 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 551)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGGGCACCAAAGAAGATGGGGGGCCCATGCCCAGTTCAGGGCCAGCTGCCCAGTGTAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 TCGGGCAC-AAAGAAGATGGGGGGCCCATGCC-AGTTCAGAGGCAGCTGCC-AGTGTAG 506
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Fax: 314 286 1800
                                                                                                                                                         Score 424; DB 7; Ler
Pred. No. 0.00e+00;
0; Mismatches 10;
                           /lab_host="DH10B"
complement(<1. .>506)
/db_xref="GDB:6044096"
150 c 158 g
      pregnant uterus"
                                                                                                                                                         Query Match
Best Local Similarity 96.9%;
Matches 463; Conservative
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AUTHORS
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/organism="Gran: mixed (see below); Vector: pT7T3D-Pac
/Note="Organ: mixed (see below); Vector: pT7T3D-Pac
(PhArmacia) with a modified polylinker; Site_1: Not I;
Site_2: ECO RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbIM, pregnant uterus
NDHED, and fetal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
/db_xref="tarkor: pcolores 260232-265223,
/clone="813186"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA456315 506 bp mRNA EST 06-JUN-1997
aa13910.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813186 3'
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HWAN);, mRNA sequence.
AA456315
92179525
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H1111er, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lay, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thelsing, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. WashG-Merck EST Project 1997, Uppublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae;
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This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
                                                                                                                                    408
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472 ACCIGCIGGIGCAGCIGCAGICCCIGGIGGGCCGGGCACTCACICIGGCAGCCGCCGICC 413
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                                         289 CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGGTCGCGAAGGCCAG
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Washbgton University School of Medicine
Washshapton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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AUTHORS
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                                                       KEYWORDS
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                                                                                                                      1. 551
/organism="Homo saplens"
/organism="Hom
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639341.123 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1410908
similar to 95:012421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN); mRNs sequence.
IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 695 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 T-GT-CGGGCACCAAAGAAGATGGGGGGCCATGCCCAGTTCAGGGCCA-GCTGCCCAGT- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.00e+00;
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complement(<1. .>551)
/db_xref="GDB:3758023"
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1 Similarity 93.5%;
491; Conservative
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/organism="Homo sapiens"
/organism="Homo sapiens"
/note='Organ: prostate; Vector: Bluescript SK-; Site_1:
Cool; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Normal prostate epithalial cell line (HPV
immortalized). 5' adaptor sequence: 5' GAATTCGGCACGAG 3'
a' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3'
Average insert size: 1.1 kb."
/db_xref="taxon:9606"
/clone="imAGE:1410908"
                                                                                                                                                                                                                                                                                                                                                                                         ph.D.

CDNA Library Preparation: Strategene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo. 1 (bases 1 to 505) NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                          Robert K. Bright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 100
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                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Teal: Robert_Strausberg@nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Pr25"
/tissue_type="epithelium (cell line)"
/lab_host="SOLR (kanamycin resistant)"
148 c 156 9 t 89 t
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 323.
Location/Qualifilers
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                                                                                                                                                                                                                                             Unpublished (1997)
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Tel: (301) 496-1558
Email: Robert_Strausberg@nlh.gov
Ph.D., Gerald Marti, M.D.
ConNa. Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/Link at:
                                                                                                    obsective 543 bp mrna EST 19-FEB-1998 obsective in No. CGAP_GCB1 Homo sapiens cDnA clone IMAGE:1338240 stanilar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR AA805072
                                                                                                                                                                                                                                                             Eukaryotae: Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 543)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                292 GGTAGTGGCTGCCGCCCCCACTGACCAGCAGGATCCACCAAGGCCCAGCCCATTTG 233
399 GGTAGTTGTCCCGCCGCCCCCACTGAC-AGCAGGAGATCCACCAAGGCCCAGGCCCATTGG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 399; DB 15; Length 543;
Pred. No. 0.00e+00;
0; Mismatches 22; Indels 7;
                                                      458 TCGGGCACCAAAGAAGGATGGGGGGCATGGCAAGTTCAGGGGCAGCTG 505
                                                                     cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:1338240"
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/tissue_type="germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 903 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 272.
Location/Qualifiers
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Best Local Similarity 94.1%;
Matches 463; Conservative
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54 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAAGCACAGGACACTGCTCCGG 113

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AA768741 507 bp mRNA EST 08-FEB-1998 ob22g01.s1 NCI_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1324464 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HMAN); mRNA sequence.
AA768741
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Frimates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 507)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                           114 GIGGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCTCGAC 173
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                                  592 GTGGGGGCTCAGGTGGGCCCACCTCTGAAGCTCTGCTGACCCCTGGGCCCAAGGCCCTGAC
                                                                    174 AGACTAGCAGGCCCAGTGGTCATGAAAGCGTGACGGCCACCACCATCACAAGCGTGATGGC
                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
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/clone="IMAGE:1324464"
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/tissue_type="2 pooled tumors (clear cell type)"
/lab.host="DH10B"
a 144 c 151 g 101 t
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                                                Query Match 60.4%; Score 394; DB 13; Length 507; Best Local Similarity 96.5%; Pred. No. 0.00e+00; Matches 435; Conservative 0; Mismatches 11; Indels
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	Scoring table: PAM 150 Gap 11		Post-processing: Minimum Match 0% Listing first 45 summaries	Database: a-geneseq31-2 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27	Statistics: Mean 31.057; Variance 140.986; scale 0.220	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.	1 100 8.5 483 20 W12135 Alpha-amylase variant 5.89e+00 4 100 8.5 483 20 W12137 Alpha-amylase variant 5.89e+00 4 100 8.5 483 20 W12137 Alpha-amylase variant 5.89e+00 5 100 8.5 483 20 W12138 Alpha-amylase variant 5.89e+00 6 100 8.5 483 20 W12139 Alpha-amylase variant 5.89e+00 7 100 8.5 483 20 W12115 Alpha-amylase variant 5.89e+00 8 100 8.5 483 20 W12115 Alpha-amylase variant 5.89e+00 9 100 8.5 483 20 W12131 Alpha-amylase variant 5.89e+00 10 10 8.5 483 20 W12131 Alpha-amylase variant 5.89e+00 11 100 8.5 485 20 W12131 Alpha-amylase variant 5.89e+00 12 100 8.5 485 20 W12131 Alpha-amylase variant 5.89e+00 13 100 8.5 485 20 W12131 Alpha-amylase variant 5.89e+00 14 100 8.5 485 20 W12131 Alpha-amylase variant 5.89e+00 15 100 8.5 485 20 W12131 Alpha-amylase variant 5.89e+00 16 100 8.5 485 20 W12121 Alpha-amylase variant 5.89e+00 17 100 8.5 485 20 W12121 Alpha-amylase variant 5.89e+00 18 100 8.5 485 20 W12121 Alpha-amylase variant 5.89e+00 19 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 19 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 19 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 19 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 10 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 10 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 11 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 12 12 13 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00 13 100 8.5 485 20 W12110 Alpha-amylase variant 5.89e+00

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W12109	M12100	W12101	W12111	W12117	W12112	W12102	W12126	W12120	W12098	W12113	WIZII4	W12120	W12100	W12099	W12105	W12106	W12103	W12107	W12119	W12132	W12122	ALIGNMENTS		44 507			C+M430C+Y	thermal s	pha-amvlo	izing; papermaking; beer-making	,		Qualifiers		1 24 3F	2510	2	Q391E		M430C		1440								•	E
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Example 3; 111pp; English.

W12099-W12144 represent alpha-amylase variants of the invention. The W12099-W12144 represent alpha-amylase variants of the invention. The W12099-W12144 represent alpha-amylase sencoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12137-W12140, and W12955, W12956, R81835 and R81836. W12137-W12140, and W12955, W12956, R81835 and R81836. W12137-W12140, and W12956, W12956, R81835 and R81836. W12137-W12140, and W12956, W12956, R81835 and R81836. W12137-W12140, and W12956, W12956, R81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability and/or reduced calcium ion dependency. The variants can also have increased alpha-amylases also be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and controlled the washing compositions, and for textile desizing.
activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of sweeteners and ethanol from starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1997 (first entry)
Alpha-amylase variant delta182 + delta184.
Alpha-amylase, detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beer-making processes. These variants can also be used in the production
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29-SEP-1995; DK-001097.
06-007-1995; DK-001121.
NOVO ) NOVO-NORDISK AS.
Bisgard-frantzen H, Borchert T, Svendsen A;
WPI; 96-371423/37.
Alpha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
                                                                                                                                                                                                           Score 100; DB 20; Length 483;
Pred. No. 5.89e+00;
8; Mismatches 10; Indels
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Pred. No. 5.89e+00;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                     43 wi-ppawkgtsqndvgygaydly-dlgefngkgtv 75
                                                                                                                                                                                                                                                                                                                                               47 WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV 80
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Best Local Similarity 40.0%;
Matches 14; Conservative
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Local Similarity 40.0%;
les 14; Conservative
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W09623873-A1.
08-AUG-1996.
05-FEB-1996; DK0056.
03-FEB-1995; DK-000126.
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ILT 3
W12137 standard; protein; 483 AA.
W12137;

RESULT ID W1 AC W1

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Example 2; 111pp; English.

W12098-W12144 represent alpha-amylase variants of the invention. The w12098-W12144 represent alpha-amylase variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases compared by W12955, W12956, R81835 and R81836. W12137-W12140, and W1243 are specifically variants of the alkaphilic Bacillus strain NCIB (12513 alpha-amylase shown in R81836. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees (clicius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylases also binding of a particular substrate. These variant alpha-amylases also coposess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and channol from starch.
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Alpha-amylase variant delta181 + delta183.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
Alpha-amylase; detergent; thermal stability; washing composition;
calcium ion dependency; alpha-amylolytic activity; washing composition;
textile desizing; papermaking; beer-making; ethanol production;
08-APR-1997 (first entry)
Alpha-amylase variant delta183 + delta184.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
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W12098-W12144 represent alpha-amylase variants of the invention. The variants of the invention were created using site directed, or random,
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stability and reduced calcium ion dependency
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Appla-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
Example 2; ; 111pp; English.
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Pred. No. 5.89e+00;
8; Mismatches 10
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05-FEB-1996; DK0056.

03-FEB-1995; DK-000126.

29-SEP-1995; DK-001097.

06-0CT-1995; DK-001097.

06-0CT-1995; DK-001131.

06-0CT-1995; DK-001121.

06-0CT-1995; DK-001121.

06-0CT-1995; DK-001121.
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29-SEP-1995; DK-001097.
06-OCT-1995; DK-001121.
00VO ) NOWO-NORDISK AS.
Bisgard-frantzen H, Borchert T, Svendsen A;
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40.0%;
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Matches 14; Conservative
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DK-000336.
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Example 2; ; 111pp; English.

W12099-W12144 represent alpha-amylase variants of the invention. The W12099-W12144 represent alpha-amylase variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12137-W12140, and W1243 are specifically variants of the alkaphilic Bacilius strain NCIB 12513 alpha-amylase shown in R81836. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees celcius), and/or vaidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values) in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of sweeteners and ethanol from starch.
mutagenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W1217-W12140, and W12143 are specifically variants of the alkaphilic Bacilius strain NCIB 12513 alpha-amylase shown in R81836. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylaylytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                              These variants can also be used in the production
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100; DB 20; Length 483;
Pred. No. 5.89e+00;
8; Mismatches 10; Indels 3; Gaps
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N W09623873-A1.
08-AUG-1996.
08-EE-1996; DK0056.
R 03-FEB-1995; DK-000126.
R 29-MAR-1995; DK-001121.
R 29-EE-1995; DK-001121.
R 06-OCT-1995; DK-001121.
R NOVO ) NOVO-NORDISK AS.
I Bisgard-frantzen H, Borchert T, Svendsen A; WPI; 96-314423/37.
T Alpha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100; DB 20; Length 483;
Pred. No. 5.89e+00;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: | || || : :|||:| : :|| || :|: |
47 WVLGPVW-GILYSAMGYGSYLVWKELGGFTEKAVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 wi-ppawkgtsqndvgygaydly-dlgefnqkgtv 75
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Alpha-amylase variant delta181 + delta182.
                                                                                                                                                                                                                                                                                                                              beer-making processes. These variants
of sweeteners and ethanol from starch.
Seguence 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .r 5
W12139 standard; protein; 483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 8.5%;
Local Similarity 40.0%;
les 14; Conservative
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Best Local Similarity 40.0%;
Matches 14; Conservative
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mitagenesis of the invention were created uning site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12137 w12140, and W12143 are specifically variants of the alkaphilic Bacillus strain NCIB (W12143 are specifically variants of the see variants can have improved thermal stability (such as at temperatures in the range of 40.70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also cossess improved specificity to a particular substrate, and/or improved cossess improved specificity to a particular substrate, and/or improved specificity and washing compositions, and for textile desizing. The used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in the production composition and washing processes. These variants can also be used in the production
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                                                                                                                                                                                                                                       08-APR-1997 (first entry)
Alpha-amylase variant delta183 + delta184 + M202L/I.
Alpha-amylase, detergent; thermal stability; oxidation stability; enzyme calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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W12098-W12144 represent alpha-amylase variants of the invention.
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40.0%; Pred. No. 5.89e+00;
vative 8; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bisgard-frantzen H, Borchert T, Svendsen A; WPI; 96-371423/37.
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                                 89
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Alpha-amylase variant delta181 + delta182
|: | | | | : : | | : | | | : | | 47 WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of sweeteners and ethanol from starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ney Location/Qualifiers misc_difference 202
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                                                                                                                                                                         standard; protein; 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
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29-WAR-1995; DK-000336.
29-SEP-1995; DK-001097.
06-OCT-1995; DK-001121.
(NOVO ) NOVO-NORDISK AS.
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DK-000336.
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08-AUG-1996.
05-FEB-1995; DK0056.
03-FEB-1995; DK-00012.
29-MAR-1995; DK-00033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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Matches
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Gaps

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43 wi-ppawkgtsqndvgygaydly-dlgefnqkgtv 75

US-09-047-652A-3.rag

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Willy Specified and evaluate - with improved thermal and oxidation stability and reduced calcium ion dependency
Stability and y. illippic Emplish.

Wil2098-Wil2144 represent alpha-amylase successor and stability and reduced, or random, and and reduced by Mil2056, Rel 18185 and Rel 1836. Mil2098-Wil2136, Wil2141, Wil2142 and Wil2142 and Wil2152, Wil2156, Rel 18185 and Rel 1836. Mil2098-Wil2136, Wil2142 and Wil2142 and Wil2142 and Wil2142 and Wil2142 and Wil2142 and Wil2152, Wil2156, Rel 1835 and Rel 1836. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8:5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved consisting and reference and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and constraint also be used in the production of sweeteners and ethanol from starch.
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PR 09-FEB-1995; DK-00126.

PR 03-FEB-1995; DK-00126.

PR 29-MAR-1995; DK-001026.

PR 29-MAR-1995; DK-001036.

PR 29-SEP-1995; DK-001036.

PR 196-5714295; DK-001037.

PR NOVO ) NOVO-NORDISK AS.

PI Bisgard-frantzen H, Borchert T, Svendsen A;

Bisgard-frantzen H, Borchert T, Svendsen A;

PT Alpha-amylase variants - with improved thermal and oxidation atebility and reduced calcium ion dependency

PT Alpha-amylase variants - with improved thermal and oxidation atebility and reduced calcium ion dependency

CC Variants of the Invention were created using site directed, or random, witagenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12098-W12098-W12136, W12098-W12136, W12098-W12136, W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098-W12098
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Alpha-amylase variant delta183 + delta184.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 8.5%; Score 100; DB 20; Length 483; Local Similarity 40.0%; Pred. No. 5.89e+00; Nes 14; Conservative 8; Mismatches 10; Indels
                                                                                      Bisgard-frantzen H, Borchert T, Svendsen A; WPI; 96-371423/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 wi-ppawkgtsqndvgygaydly-dlgefnqkgtv 75
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W12116 standard; protein; 483 AA.
                                                       (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
WO9623873-A1.
                           06-OCT-1995;
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Stample 2; ;111pp; English.

M1209-W12144 represent alpha-amylase variants of the invention. The w1209-W12144 represent alpha-amylase variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141, W12142 and W12144 are specifically variants of the alkaphilic Bacillus train NCIB 12512 alpha-amylase shown in R81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or reduced calcium ion dependency. The variants can also have increased alpha-amylases also crivity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate. These variant alpha-amylases can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of a particular substrate and washing can also be used in papermaking and beer-making processes. These variants can also be used in the production of a particular substrate and washing can also be used in the production of a particular substrate. These variants can also be used in the production are considered to the starch.
The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of sweeteners and ethanol from starch. Sequence 483 AA;
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                                                                                                                                                                                                                                                                                                                                                                    08-APR-1997 (first entry)
Alpha-amylase variant L351C + M430C + delta183 + delta184.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
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                                                                                                                                                          Gaps
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                                                                                                               Length 483;
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                                                                                                          Score 100; DB 20; Length 48:
Pred. No. 5.89e+00;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100; DB 20; Length 48:
Pred. No. 5.89e+00;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1995; DK-000336.
29-SEP-1995; DK-001097.
06-OCT-1995; DK-001121.
010VO ) NOVO-NORDISK AS.
Bisgard-frantzen H, Borchert T, Svendsen A;
                                                                                                                                                                                              43 w1-ppawkgtsqndvgygaydly-dlgefngkgtv 75 l: | | | | : :|||:| | :| | 47 WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: | | | | : : | | | : | | | 47 WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 wi-ppawkgtsqndvgygaydly-dlgefnqkgtv 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ney
misc_difference 351
                                                                                                                                                                                                                                                                                                                                standard; protein; 483 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label = L351C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= M430C
                                                                                                          Query Match 8.5%;
Best Local Similarity 40.0%;
Matches 14; Conservative
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8.5%;
Best Local Similarity 40.0%;
Matches 14; Conservative
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DK-000336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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W12133 s
W12133;
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Key Location/Qualifiers misc_difference 194
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W31499 standard; protein; 485
W31499;
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Best Local Similarity 40.0%;
Matches 14; Conservative
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(NOVO ) NOVO-NORDISK AS
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DK-000336.
DK-001097.
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29-SEP-1995;
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Matches
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W12098-W12144 represent alpha-amylase variants of the invention. The W12098-W12144 represent alpha-amylase variants of the invention were created using site directed, or random, mutagenesis of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases or represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141, W12144 and W12144 are specifically variants of the alkaphilius strain NCIB 12512 alpha-amylase shown in R81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or caidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also be ossess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be alpha-amylase variants can also be used in papermaking and beer making processes. These variants can also be used in the production of the alpha-amylase variants can also be used in the production of the alpha-amylase variants can also be used in the production of the alpha-amylase variants can also be used in the production of the content of the co
08-APR-1997 (first entry)
Alpha-amylase variant Ri24P + delta183 + delta184.
Alpha-amylase, detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Claim 1; Pages 88-89; 97pp; English.
The present sequence is a Bacillus sp. alpha amylase with a specific activity at least 25% higher than that of Termamyl (RTM) at 25 to 55 degrees C at pH 8 to 10, measured by the Phadebas (RTM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 8.5%; Score 100; DB 20; Length 483; Local Similarity 40.0%; Pred. No. 5.89e+00; les 14; Conservative 8; Mismatches 10; Indels 3
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W31500;
08-APR-1998 (first entry)
8acillus sp. alpha amylase.
Bacillus sp.
W09732961-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-1995; DK0056.
03-FEB-1995; DK-000126.
29-MAR-1995; DK-000336.
29-EBP-1995; DK-0011097.
06-OCT-1995; DK-001121.
(NOVO) NOVO-NORDISK AS.
WPI; 96-371423/37.
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47 WVLGPVW-GTLYSAMGYGSYLVWKELGGFTEKAVV 80
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- R124P
                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference 12
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                                                                                                                                                                                                                                                                                                                            Synthetic.
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Sequence Query Match Matches

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M8-APR-1997 (first entry)
Alpha-amylase variant E1940.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
Alpha-amylase; detergent; thermal stability; washing composition;
calcium ion dependency; alpha-amylolytic activity; washing composition;
textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The state of the s
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activity test. It is of use in hard surface cleaning, hand or machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care are obtained by using it at a concentration of 0.00018 to 0.06% sequence 485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp. alpha amylase.
Alpha amylase; hard surface cleaning; dishwashing; laundry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches 10;
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Pred. No. 5.89e+00;
8; Mismatches 10
                                                                                                                                                                                                                                                                                                                                       8.5%; Score 100; DB 27;
Local Similarity 40.0%; Pred. No. 5.89e+00;
hes 14; Conservative 8; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 wi-ppawkgtsqndvgygaydly-dlgefnqkgtv 75
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                                                  Tablility and reduced calcium ion dependency
Claim 11: 111pp: English.
W12098-W12144 represent alpha-amylase variants of the invention. The
W12098-W12144 represent alpha-amylase variants of the invention were created using site directed, or random,
mutagenesis of the invention were created using site directed, or random,
crepresented by W12955, W12956, R81835 and R81836. W12099-W12136, W12141,
W12142 and W12144 are specifically variants of the alkaphilic Bacillus
crepresented by W12955, W12956, R81835 and R81835. These variants can have
improved thermal stablility (such as at temperatures in the range of 40-70
degrees Celcius), and/or oxidation stablility, and/or reduced calcium ion
dependency. The variants can also have increased alpha-amylolytic
critivity (especially at pH values in the range of 8.5-10.5), and improved
binding of a particular substrate. These variant alpha-amyloses also
bossess improved specificity to a particular substrate, and/or improved
specificity with respect to cleavage of Substrate. These sequences can
be used in detergent and washing compositions, and for textile desizing.
The alpha-amylase variants can also be used in papermaking and
c sweeteners and ethanol from starch.
Sequence 485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 11; illipp; English.

W12098-W12144 represent alpha-amylase variants of the invention. The variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases controlled will be parent alpha-amylases represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141, W12142 and W12144 are specifically variants of the alkaphilius Bacilius strain NCIB 12512 alpha-amylase shown in R81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylases also binding of a particular substrate. These variant alpha-amylases also pecificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-1997 (first entry)
Alpha-amylase variant N106D.
Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
Alpha-amylase; detergent; thermal stability; washing composition;
calcium ion dependency; alpha-amylolytic activity; washing composition;
textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100; DB 20; Length 485;
Pred. No. 5.89e+00;
8; Mismatches 10; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-AUG-1996.
05-FEB-1995; DK-000126.
29-MAR-1995; DK-000126.
29-SEP-1995; DK-000336.
29-SEP-1995; DK-001097.
06-OCT-1995; DK-001071.
06-OCT-1995; DK-001078; AS.
Bisgard-frantzen H, Borchert T, Svendsen A;
WPI: 96-371433/37.
Alpha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
                                        Alpha-amylase variants - with improved thermal and oxidation
Bisgard-frantzen H, Borchert T, Svendsen A;
WPI; 96-371423/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Best Local Similarity 40.0%;
Matches 14; Conservative
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The alpha-amylase variants can also be used in papermaking and beer-making processes. These variants can also be used in the production of sweeteners and ethanol from starch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or beer making claims, particle described by having a specific claim 5; Page 46-48; 65pp; English.

This alpha-amylase protein is characterized by having a specific activity at least 25% higher than the specific activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme can be used in detergent composition for starch liquefaction, the production of lignocellulosic materials, e.g. pulp, paper and cardboard from waste containing starch, for deinking recycled starch-coated, or starch-containing spinted apper, to modify starch for papermaking, for textile desizing, and beer-making processes. This protein may be produced recombinantly.
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1996 (first entry)
Bacillus sp. alkaline alpha-amylase.
Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile; beer; starch.
                                                                                                                                          Score 100; DB 20; Length 485;
Pred. No. 5.89e+00;
8; Mismatches 10; Indels 3;
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Bisgard-Indicate H. Ostergaard PR., Outtrup H., Rasmussen MD; Van DER ZEE P.
WPI, 95-351318/45.
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Local Similarity 40.0%; Pred. No. 5.89e+00;
tes 14; Conservative ...
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                                                                                                                                                                                                                                                                                                                                                                                    LT 15
R81836 standard; protein; 485 AA.
R81836;
                                                                                                                                          Query Match
Best Local Similarity 40.0%;
Matches 14; Conservative
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29-MAR-1995; DK0142.
29-MAR-1994; DK-000353.
03-NOV-1994; DK-001271.
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US-09-047-652A-3.rpr

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Jul 21 14:53:23 1998; MasPar time 10.79 Seconds 572.052 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-047-652A-3 (1-169) from US09047652A.pep 1170 1 XXXXXXXXXXXXXXXXXXXXXIII Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 41.783; Variance 103.237; scale 0.405 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Pred No.	•	3.12e-17	1.75e-14	3.93e-14	2.75e-14	1.04e-13	1.10e-13	2.20e-34	1.60e-32	1.94e-29	5.41e-27	3.98e-15	4.83e-08	3.58e-04	2.33e-02	3.28e-01	3.28e-01	7.08e-01	7.08e-01	9.12e-01	1.17e+00	1.17e+00	1.17e+00	2.48e+00
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1		S14257	IS7953	JC1393	A53405	138105	A39473	S04404	B69434	A57438	S49622	I48082	669987	S76477	845776	C47755	S75962	S70680	S77220	D64800	669897	A45831	A64763	JC4832
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Length		169	169	169	169	169	169	160	153	158	157	31	155	159	639	283	634	188	282	246	292	368	418	271
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157953 #type complete
peripheral-type benzodiazepine receptor - mouse
#formal_name Mus musculus #common_name house mouse
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
157953
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ACCESSIONS REFERENCE

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RESULT ENTRY TITLE ORGANISM DATE

3 518 1 A27705 alpha-amylase (EC 3.2 2.48e+00 637 2 525330 SCT1 protein - yeast 5.16e+00 213 2 525330 SCT1 protein - yeast 8.16e+00 213 2 5215413 ORF - African claved 8.35e+00 653 2 002339 omega-3 fatty acid de 6.57e+00 677 2 51579 cmoga-3 fatty acid de 6.57e+00 677 2 51579 cmoga-3 fatty acid de 6.57e+00 670 2 569146 heme exporter protein 1.06e+01 68 245 2 564989 heme exporter protein 1.06e+01 68 25 2 002336 hypothetical protein 1.34e+01 7 226 2 577370 surface antigen - hep 1.34e+01 7 332 2 577370 surface antigen - hep 1.34e+01 7 478 2 564895 surface antigen - hep 1.34e+01 7 478 2 525155 hypothetical protein 1.34e+01 8 252023 surface antigen - hep 1.70e+01 8 26401 8 26401 surface antigen - hep 1.70e+01 8 26401 8 26401 surface antigen - hep 1.70e+01 8 26401 8 26401 surface antigen - hep 1.70e+01 8 26401 8 26401 surface antigen - hep 1.70e+01 8 26401 8 26401 surface antigen - hep 1.70e+01 8 26401 8 26401 surface antigen - hep 1.70e+01 8 26401 8 26401 Surface antigen - hep 1.70e+01 8 26401 8 26401 8 26401 Surface antigen - hep 1.70e+01 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 26401 8 264	#type complete azepine receptor, peripheral-type - huname Homo sapiens #common_name man 1994 #sequence_revision 10-Nov-1995 #t. r-1998  J.; Mattei, M.G.; Kaghad, M.; Dumont, le Fur, G.; Caput, D.; Ferrara, P. Blochem. (1991) 195:305-311 ar cloning and chromosomal localization heral-type benzodiazepine receptor. D:91146565 eliminary NA NA NA ABA GE:M36035; NID:9184333; PID:9306883 ndrion; transmembrane protein	tch al Similarity 98.6%; Score 1160; DB 2; Length 169; al Similarity 98.6%; Pred. No. 3.12e-170; 141; Conservative Mismatches 0; Indels 0; Gaps 0; HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYT 86 HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYT 86 GGLALNWAWPPIFFGARQMGWALVDLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAF 146 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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##cross-references GB:J05122; NID:g206161; PID:g206162
r This protein is located mainly in the mitochondrial outer membrane.
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Garnier, M.; Dimchev, A.B.; Boujrad, N.; Price, J.M.; Musto,
N.A.; Papadopoulos, V.
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th 169 #molecular-weight 18940 #checksum 5649
                                                                                                                                                                                                                                                                                                27 HGEGLRWYAGLOKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYT 86
                       #journal Mol. Pharmacol. (1994) 45:201-211
#title In vitro reconstitution of a functional peripheral-type
benzodiazepine receptor from mouse Leydig tumor cells.
#cross-references MUID:94158796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            benzodiazepine receptor, mitochondrial - rat
peripheral-type benzodiazepine receptor PKBS
#formal_name Rattus norvegicus #common_name Norway rat
30-8ep-1993 #sequence_revision 30-Sep-1993 #text_change
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#fresidues 1-169 ##label CAS
##cross-references GB:M84221; NID:g206478; PID:g206480; GB:M95864
NCE A32680
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                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 1.75e-144;
12; Mismatches 10; Indels
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##cross-references GB:L17306; NID:q309441; PID:q309442
##cross-references Handlecular-weight 18841 #check
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Query Match

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J. Biol. Chem. (1994) 269:7527-7531 Induction of peripheral-type benzodiazepine receptors during differentiation of mouse erythroleukemia cells. A possible involvement of these receptors in heme blosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. (1994) 269:2527-7531 Induction of peripheral-type benzodiazepine receptors during differentiation of mouse erythroleukemia cells. A possible involvement of these receptors in heme biosynthesis.
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                                                                                                                                                                                                             ##residues 1-169 ##label TAK ##cross-references GB:D21207; NID:9484053; PID:d1005281; PID:9484054
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                                                                                                     27 RGEGLRWYASLQKPSWHPPRWTLAPIWGTLYSAMGYGSYIIWKELGGFTEEAMVPLGLYT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A53405 #type complete
peripheral-type benzodlazepine receptor 1
isoquinoline-binding protein - mouse
fromal_name Mus musculus #common_name house mouse
12-May-1994 #sequence_revision 12-May-1994 #text_change
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                           0; Gaps
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Comparison of repetitive elements in the third intron human and rodent mitochondrial benzodiazepine
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#length 169 #molecular-weight 18829 #checksum
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Pred. No. 2.75e-142;
14; Mismatches 10; Indels
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                              Indels
Pred. No. 3.93e-143;
14; Mismatches 10;
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#cross-references MUID:95237610
#accession I49099
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A53405; I55415; I49099
                                                                                                                                                                                                                                                                                          147 ATMLNYYVWRDNSGRRGGSRLTE 169
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Best Local Similarity 83.2%;
Matches 119; Conservative
Local Similarity 83.2%;
nes 119; Conservative
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##residues 1-16
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##residues 95-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Parola, A.L.; Stump, D.G.; Pepperl, D.J.; Krueger, K.E.;
    Regan, J.W.; Laird II, H.E.
    *journal J. Biol. Chem. (1991) 266:14082-14087
#title Cloning and expression of a pharmacologically unique bovine peripheral-type benzodiazepine receptor isoquinoline binding protein.
#cross-references MUID:91310699
                                                                                                                                                                                                                                                                                cloning
and characterization of alternative splicing in normal tissues and in a patient with congenital lipoid adrenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 WAAGPELGMA-PHLL-GARQMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLG-LY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVGSPGPLH 86
                                                                                                          peripheral benzodiazepine receptor - human formal_name Homo sapiens #common_name man 24-May-1996 #sequence_revision 24-May-1996 #text_change 138105
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#formal_name Bos primigenius taurus #common_name cattle
27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                        61/2; 107/3
#length 169 #molecular-weight 18483 #checksum 2466
                                                                                                                                                                                                                                                Lin, D.; Chang, Y.J.; Strauss, J.F.; Miller, W.L. Genomics (1993) 18:643-650
The human peripheral benzodlazepine receptor gene:
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Pred. No. 1.04e-135;
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                                                                        147 ATVLNYYVWRDNSGRRGGSRLAE 169
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Local Similarity 86.2%;
hes 125; Conservative
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A39473
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##residues 1-1
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Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.
Mol. Gen. Genet. (1989) 216:254-268
Nucleotide sequence, organization, and nature of the protein
products of the carotenoid biosynthesis gene cluster of
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                                                                                                                                                                                                                                                   87 ILWIPIFFGLHRLAGGMLVLVLLMLSVFATCVLFWSVDWLSG-LMFVPYVIWVTVAGALN 145
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                                                                                                                                                                                   27 RGEGFRWYASLQKPPWHPPRWILAPIWGTLYSAMGYGSYMIWKELGGFSKEAVVPLGLYA 86
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                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S04404 #type complete
crtK protein - Rhodobacter capsulatus
#formal_name Rhodobacter capsulatus
28.Feb-1990 #sequence_revision 28.Feb-1990 #text_change
09-Sep-1997
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05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change
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#length 160 #molecular-weight 17608 #checksum
                      #checksum
                                                               Score 944; DB 2; Length 169;
Pred. No. 1.10e-133;
24; Mismatches 11; Indels
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Pred. No. 2.20e-34;
35; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-160 ##label ARM
##cross-references EMBL:X52291; NID:945996; PID:946000
                   #molecular-weight 18927
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#cross-references MUID:89313663
transmembrane protein
#length 169 #molecula
                                                                                                                                                                                                                                                                                                                                                   147 AGMLNYRMWQDNQVRRSGRRLSE 169
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147 TTTLNYCVWRDNHGWRGGRRLPE 169
                                                               80.7%;
llarity 75.5%;
Conservative
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Best Local Similarity 37.2%;
Matches 48; Conservative
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152 YCVWRDNHG 160
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D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.;
Lue, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.;
Peterson, S.; Relch, C.I.; McNeil, L.K.; Badger, J.H.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman,
J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs,
T.; Artiach, P.; Raine, B.P.; Sykes, S.M.; Sadow, P.W.;
D'Andrea, K.P.; Bowman, C.; Fujil, C.; Garland, S.A.;
Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
C.R.; Venter, J.C.
sulfate-reducing archaeon Archaeoglobus fulgidus.
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Yeliseev, A.A.; Kaplan, S.
J. Biol. Chem. (1995) 270:21167-21175
A sensory transducer homologous to the mammalian peripheral-type benzodiazepine receptor regulates photosynthetic membrane complex formation in Rhodobacter sphaeroides 2.4.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptophan-rich sensory protein - Rhodobacter sphaeroides
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26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change
26-Jan-1996
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#length 158 #molecular-weight 17976 #checksum 9469
                                                                                                                                                                                                                                                                                                                                   preliminary; nucleic acid sequence not shown;
translation not shown
                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-153 ##label KLE
##cross-references GB:AE000782; TIGR:AF1475
X #length 153 #molecular-weight 17185 #checksum 36
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Pred. No. 1.94e-29;
29; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 327; DB 2; Length 153
Pred. No. 1.60e-32;
30; Mismatches 39; Indels
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Best Local Similarity 39.0%;
Matches 48; Conservative
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Best Local Similarity 38.3%;
Matches 46; Conservative
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##molecule_type DNA
##residues 1-1
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                                                                                                                                               Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N. submitted to the EMBL Data Library, November 1994 and The complete DNA sequence, specific TNS insertion map and gene assignment of the carotenoid biosynthesis genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 ILWIPVFFGMKRMATALAVVMVMWLFVAATMWAFFQLDTWAGVLFVPYLIWATAATGLNF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 WYDNLNKPWWNPPRWVFPLAWTSLYFLMSLAPC-GWR--SS-KVRAGAGL-LCA-QLAFN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 WYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYTGQLALN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E.
Gene (1995) 155:201-205
Comparison of repetitive elements in the third intron of
human and rodent mitochondrial benzodiazepine
   849622 #type complete
crtK protein - Rhodobacter sphaeroides
#formal_name Rhodobacter sphaeroides
05-Mar-1995 #sequence_revision 12-May-1995 #text_change
09.Sep-1997
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mitochondrial benzodiazepine receptor - Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                        #length 157 #molecular-weight 17854 #checksum 6363
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##residues
#### 1-31 ##1-2-
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                                                                                                                                                                                                                                                                                           Score 291; DB 2; Length 157,
Pred. No. 5.41e-27;
28; Mismatches 42; Indels
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#length 31 #checksum 7498
                                                                                                                                                                                                                          Rhodobacter sphaeroides.
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#cross-references MUID:95237610
                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues
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Best Local Similarity 36.7%;
Matches 44; Conservative
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RESULT

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25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Sep-1997

\$76477 \$type complete hypothetical protein - Synechocystis sp. (PCC 6803) \$formal_name Synechocystis sp.

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##status
##molecule_type DNA
##cosstdues 1-159 ##label KAN
##cross-references EMBL:D90915; NID:g1653604; PID:d1019339; PID:g1653694
##cross-references EMBL:D90915; NID:g1653604; PID:d1019339; PID:g1653694
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
                                                                                                                                                                                                                                                              #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamcto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Marati, A.; Nakazaki, N.; Matuo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

#journal Na Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6603. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
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MARY #length 159 #molecular-weight 17809 #checksum 1905
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Best Local Similarity 25.0%;
Matches 30; Conservative
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                                                                                                                                                                                            Augusta, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, P.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Bouusler, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Braun, M.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Braun, M.; Choi, S.M.; Codmerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Densterhoeft, A.; Ebritch, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Eabret, C.; Ferrar, E.; Foulger, D.; Fritz, C.; Fulita, M.; Fulita, Y.; Funa, S.; Gallacin, B.J.; Grandi, G.; C.; Ferrar, A.; Hilbert, M.; Gallech, J.; Harwood, C.R.; Henatch, A.; Hilbert, M.; Holseppl, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kurita, K.; Lapidus, M.; Jones, L.; Joris, B.; Karamata, D.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Rasahara, Y.; Rlaerr-Blanchard, M.; Relle, C.; Robayashi, Y.; Roetter, P.; Koningstein, G.; Kroph, S.; Kamano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Perscott, M.; Poph, T.M.; Popher, M.; Ogiwa, K.; Ogiwar, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Rapoport, G.; Roche, B.; Rose, M.; Sadle, Y.; Scalo, B.; Brak, M.; Brose, M.; Sadle, Y.; Scalo, S.; Schleich, S.; Schocke, B.; Shi, M.; Tamakoshi, H.; Tarkemaru, R.; Tarkemaru, R.; Tarkemeru, R.; Wedler, H.; Weller, H.; Waltzenegger, T.; Wanters, P.; Wippt, A.; Yanneller, B.; Wanter, R.; Wanter, M.; Wanter, R.; Wanter, M.; Wanter, M.;
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bypothetical protein ytaB - Bacillus subtilis #formal_name Bacillus subtilis 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; nucleic acid sequence not shown;
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Gaps

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Score 130; DB 2; Length 159 Pred. No. 3.58e-04; 30; Mismatches 55; Indels

nucleic acid sequence not shown; translation not shown

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Skalā, J.; Goffeau, Ā.
Yeast (1994) 10:1489-1496
The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome II reveals homologues to bacterial proline synthetase and murine alpha-adaptin, as well as a new permease and a DNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Wergifosse, P.; Jacques, B.; Jonniaux, J.L.; Purnelle, B.;
                                                                                                                                                                                                                                                                                                                 ##residues 1-639 ##label GOF ##cross-references EMBL:23803; NID:9536058; PID:9536059; MIPS:YBL042c ##experimental_source strain S288C S50284
                                                                                                                                                                                                    $45745
Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de
Wergifosse, P.; van Dyck, L.
submitted to the Protein Sequence Database, August 1994
$45776
S45776 #type complete
uracil transport protein homolog YBL042c - yeast
(Saccharomyces cerevisiae)
protein YBL0406
#formal_name Saccharomyces cerevisiae
26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change
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S45776; S50783
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##molecule_type DNA

89 QAFSYFOFTOKNLLAASLDCLLVAITAIVLLIIAKKYSRAASYLLLPYFLWSAFATFLSF 148

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Lindeberg, M.; Collmer, A.
J. Bacteriol. (1992) 174:7385-7397
Analysis of eight out genes in a cluster required for pectic enzyme secretion by Exwinia chrysanthemi: sequence comparison with secretion genes from other gram-negative
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pectic enzyme secretion protein OutO - Erwinia chrysanthem1
#formal_name Erwinia chrysanthem1
24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change
C47755
A47021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TGLQLGLNW-WQT-WICIW-VGYTFVAFFLILGSKVGNN---YHISFPISSRVSFGIYFS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *sequence extracted from NCBI backbone (NCBIP:118281)
*superfamily hypothetical protein b2972
transmembrane protein
#length 283  #molecular-weight 31355  #checksum 9186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 115; DB 2; Length 639;
Pred. No. 2.33e-02;
26; Mismatches 26; Indels 10; Gaps
                                                                                                                                                                                                                     #domain transmembrane #status predicted #label TMA
#domain transmembrane #status predicted #label TMA
#domain transmembrane #status predicted #label TMA
#domain transmembrane #status predicted #label TMS
#domain transmembrane #status predicted #label TMI
#length 639 #molecular-weight 72164 #checksum 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          э
Э
##residues 1-639 ##label DEW
##cross-references EMBL:X78214; NID:9463261; PID:9872301
##experimental_source strain S288C
                                                                                                                                                                                                      predicted
predicted
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9.0%; Score 105; DB 2; Length 283;
Best Local Similarity 26.4%; Pred. No. 3.28e-01;
Matches 14; Conservative 23; Mismatches 13; Indels
                                                                                                                                                                            predicted
                                                                                                                                                                            #status
                                                                                                                                                                                                 transmembrane
                                                                                                                       transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 IWIVINRVVMACVWNSTLAYIGSQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteria.
#cross-references MUID:93054355
#accession C47755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.2%;
Matches 22; Conservative
                                                                                                #map_position 2L
KEYWORDS tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##note
CLASSIFICATION
KEYWORDS
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSIONS
REFERENCE
#authors
#journal
#title
                                                                                                                                                                                                                                                                                          332-348
364-393
417-433
460-478
482-5503
537-554
570-590
SUMMARY
                                                                                                                                                                     162-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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Search completed: Tue Jul 21 14:53:50 1998 Job time: 27 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.91 Seconds 613.189 Million cell updates/sec Tue Jul 21 14:54:08 1998; Run on:

Tabular output not generated.

>US-09-047-652A-3 (1-169) from US09047652A.pep 1170 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 segs, 25083644 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot35 1:swiss1 Database:

Mean 43.233; Variance 89.342; scale 0.484 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 1160 2 10008 3 3 10008 5 3 3 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	288886 2805 2905 2006 2006 2006	169 169 169			Coor Present	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
нн	2888 2000 2000 2000 2000 2000 2000 2000	169	Н	PKBS_HUMAN	PERIPHERAL-TYPE BENZOD	3.59e-203
н	2895 290.5 200.5 200.5 200.5	169		PKBS_MOUSE	PERIPHERAL-TYPE BENZOD	1.94e-172
	20.0 20.0 20.0 20.0 20.0 20.0			PKBS_RAT	PERIPHERAL-TYPE BENZOD	7.93e-171
	0,0000 0,000 0,000 0,000	169	-	PKBS_BOVIN	PERIPHERAL-TYPE BENZOD	1.48e-159
	0 0 0 0 0 0 0 1	160	-	CRTK_RHOCA	CRIK PROTEIN.	3.11e-41
	0 8 0 0 6 n	639	-	YBE2_YEAST	PUTATIVE TRANSPORTER Y	2.22e-03
	00 0 10 11	283	Н	LEP3_ERWCH	TYPE 4 PREPILIN-LIKE P	4.81e-02
	a	246	-	GLTJ_ECOLI	GLUTAMATE/ASPARTATE TR	1.58e-01
		418		MHPT_ECOLI	PUTATIVE 3-HYDROXYPHEN	2.11e-01
	8 . 9	271		CDSA_PSEAE	PHOSPHATIDATE CYTIDYLY	5.01e-01
	8.3	518		AMT6_BACS7	GLUCAN 1,4-ALPHA-MALTO	5.01e-01
	8.1	447		FD3C_SESIN	OMEGA-3 FATTY ACID DES	8.83e-01
	8.1	583		FUR4_SCHPO	URACIL PERMEASE.	8.83e-01
	8.0	759		SCT1_YEAST	CTR1 SUPPRESSOR PROTEI	1.17e+00
	7.9	213	-	IF4E_XENLA	EUKARYOTIC TRANSLATION	2.03e+00
16 92	7.9	263	-	CCMC_BRAJA	HEME EXPORTER PROTEIN	2.03e+00
	7.9	453	-	FD3C_SOYBN	OMEGA-3 FATTY ACID DES	1.54e+00
18 92	7.9	677	-	BETT_ECOLI	HIGH-AFFINITY CHOLINE	2.03e+00
o	7.8	245	-	CCMC_ECOLI	HEME EXPORTER PROTEIN	2.68e+00
	7.8	438	-	FUMC_SULSO	FUMARATE HYDRATASE CLA	2.68e+00
21 91	7.8	446	-	FD3C_ARATH	OMEGA-3 FATTY ACID DES	2.68e+00
	7.8	498	-	OUSA_ERWCH	OSMOPROTECTANT UPTAKE	2.68e+00
23 90	7.7	434	-	YNM8_YEAST	HYPOTHETICAL 50.2 KD P	3.51e+00

Length 169;

Score 1160; DB 1; I Pred. No. 3.59e-203;

99.1%; 98.6%;

Query Match Best Local Similarity

2

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TRANSMEM
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                                                                                                                                                                                                                                 87 GOLALIWAMPPIFFGARQMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAF 146
                                                87 GQLALNWAWPPIFFGARQMGWALADLLLVSGVATATTLAWHRVSPPAARLLYPYLAWLAF 146
                                                                                                                                                                                                                                                                                                                                                                                                                        27 HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYT 86
                    27 RGEGLRWYASLQKPSWHPPRWTLAPIWGTLYSAMGYGSYIVWKELGGFTEDAMVPLGLYT 86
 0; Gaps
                                                                                                                     POCT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PRRIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches 10; Indels 0; Gaps
                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                TIŜSUE-TESTIS;
MEDLINE; 94158796.
GARNIER M., DIMCHEV A.B., BOUJRAD N., PRICE J.M., MUSTO N.A.,
                                                                                                                                                                                                                                                                                                                                                           Score 1008; DB 1; Length 169; Pred. No. 1.94e-172;
 0; Indels
                                                                                                                                                                                                                                                                                                            TM1 (POTENTIAL).
TM2 (POTENTIAL).
TM3 (POTENTIAL).
TM4 (POTENTIAL).
TM5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              C642B263 CRC32;
 Mismatches
                                                                                                            169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AA.
                                                                                                                                                                                                                                                                                                     RECEPTOR; TRANSMEMBRANE
                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
5,
                                                                                                                                                                                                                            45:201-211(1994).
                                                                  147 ATTLNYCVWRDNHGWHGGRRLPE 169
                                                                          147 ATVLNYYVWRDNSGRRGGSRLPE 169
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67
100
126
155
18841 MW; (
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PKBS_TAT STANDARD;
PKG257;
01-AUG-1990 (REL. 15, CREATED)
                                                                                                                                                                                                                                                                                                                                                           86.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                  84.68;
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                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                             169 AA;
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                    PAPADOPOULOS V.;
MOL. PHARMACOL.
                                                                                                                                                                                                                                                                                                    MITOCHONDRION;
                                                                                              2
PKBS_MOUSE
P50637:
                                                                                                                                                          BZRP OR MBR
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TRANSMEM
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SEQUENCE
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Matches
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GENE 121:377-382(1992).

-I-FUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE
BENZODIAZEPINE RECGNITION SITES AND IS MOST LIKELY TO COMPRISE
BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINGLINE CARBOXAMIDES.

-I-SUBCELLULAR LOCATION: MITOCHONDRION; INTEGRAL MEMBRANE PROTEIN.

-I-SUBCELLULAR LOCATION: MITOCHONDRION; INTEGRAL MEMBRANE PROTEIN.

-I-SUBCELLULAR SEGMENTS TM1, TM4, AND TM5 SHOW SIMILARITY WITH THE TRANSMEMBRANE SEGMENTS M1, M2, AND M4 FROM SUBUNITS OF THE GABA(A)/PENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.

EMBL; M44221; G206480; -.

PIR; A22680; A32680.

PIR; C01393; JC1393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 GQLALNWAWPPIFFGARQMGWALVDLMLVSGVATATTLAWHRVSPPAARLLYPYLAWLAF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 GQLALNWAWPPIFFGARQMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGEGLRWYASLQKPSWHPPRWTLAPIWGTLYSAMGYGSYIIWKELGGFTEEAMVPLGLYT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                     (PKBS) (MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (ISOQUINOLINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASALOTII S.O., PELAIA G., YAKOVLEV A.G., CSIKOS T., GRAYSON D.R.
                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-ADRENAL GLAND;
MEDLINE; 90062173.
SPRENGEL WERNER P., SEEBURG P.H., MUKHIN A.G., SANTI M.R.,
GRAYSON D.R., GUIDOTTI A., KRUEGER K.E.;
J., BIOL. CHEM. 264:20415-20421(1989).
                                                                                                       RATTUS NORVEGICUS (RAT).
EUKRRYOTA: WEFAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA;
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1000; DB 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 7.93e-171;
14; Mismatches 10;
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR)
BENZODIAZEPINE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TM1 (POTENTIAL).
TM2 (POTENTIAL).
TM3 (POTENTIAL).
TM4 (POTENTIAL).
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1C22C453 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 ATMLNYYVWRDNSGRRGGSRLTE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 BE TW 26 TW 67 TW 100 TW 126 TW 1155 TW 18940 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 85.5%;
1 Similarity 83.2%;
119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING PROTEIN) (IBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
106
135
169 AA;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-WISTAR; MEDLINE; 93077057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION;
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PKBS_BOVIN
P30535;
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TRANSMEM
TRANSMEM
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TRANSMEM
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87 ILWTPIFFGLHRLAGGMLVLVLLWLSVFATCVLFWSVDWLSG-LMFVPYVIWVTVAGALN 145
                                                                                                                                                             93 WAWPPIFFGAROMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLY-PYLAWLAFTTTLN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 TGLOLGLNW-WQT-WICIW-VGYTFVAFFLILGSKVGNN---YHISFPISSRVSFGIYFS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEP3_ERWCH STANDARD; PRT; 283 AA.
P31711;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 32, LAST SEQUENCE UPDATE)
01-NV-1995 (REL. 32, LAST SEQUENCE UPDATE)
TYPE 4 PREPILIN-LIKE PROTEIN SPECIFIC LEADER PEPTIDASE (EC 3.4.99.-)
(PECTIC ENZYMES SECRETION PROTEIN OUTO).
                                                            28 WYDSLKKPSWVPPNWLFPVAWSTLYILMSISAARV-SGLAMENELAVLGLAFWAVQIAVN 86
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C;
MEDLINE; 95176707.
DE WERGIFOSSE P., JACQUES B., JONNIAUX J.L., PURNELLE B., SKALA J.,
                    ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115; DB 1; Length 639;
Pred. No. 2.22e-03;
26; Mismatches 26; Indels 10;
  Pred. No. 3.11e-41;
35; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEAST 10:1489-1496(1994).

-1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1 - SIMILARITY: BELOCATION: OTHE ALLANTOIN PERMEASE FAMILY.
EMBL: X78214; 6872301; -.
EMBL: X35803; 6536059; -.
PIR: S45776; S45776.
HYPOTHETICAL PROTEIN: TRANSMEMBRANE; TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YBL042C OR YBL0406.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72165 MW; FBD28445 CRC32;
                                                                                                                                                                                                                                                                                                                                                                          01-077-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PUTATIVE TRANSPORTER YBL042C.
                                                                                                                                                                                                                                                                                                                                           639 AA.
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 -WLAFITILNYCVWRDNHGWRGGR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 26.2%;
les 22; Conservation
Best Local Similarity 37.2%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
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538
573
639 AA;
                                                                                                                                                                                                                     146 FSVWRLNPG 154
                                                                                                                                                                                                                                                          152 YCVWRDNHG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         YBE2_YEAST
P38196;
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TRANSMEM
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ID LE
AC P3
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DT 01
DE T1
GN 01
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                               PAROLA A.L., STUMP D.G., PEPPERL D.J., KRUEGER K.E., REGAN J.W.,
LAIRD H.E. II;
J. BIOL. CHEM. 266:14082-14087(1991).

J. BIOL. CHEM. 266:14082-14087(1991).

FUNCTION: RESPONSTBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE
BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE
BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXAMIDES.

SUBCELLULAR LOCATION: INTEGRAL MEMBANE PROTEIN.

FRANSMEMBRANE SEGMENTS MI, TM4, AND TM5 SHOW SIMILARITY WITH THE
GRADA(A)/PENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.

GRADA(A)/PENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.

EMBL, M64520; G163489; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOLALNWAWPPLFFGTROMGWALVDLLLTGGMAAATAMAWHQVSPPAACLLYPYLAWLAF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 RGEGFRWYASLOKPPWHPPRWILAPIWGTLYSAMGYGSYMIWKELGGFSKEAVVPLGLYA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S04404; S04404.

PUPOOSYNTHESIS; CHLOROPHYLL BIOSYNTHESIS; CAROTENOID BIOSYNTHESIS; TRANSMEBRANE.

TRANSMEM 3 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
-!- SIMILARITY: TO HUMAN MITOCHONDRIAL BENZODIAZEPINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 944; DB 1; Le
Pred. No. 1.48e-159;
                                                                                                                                                                                                                                                                                                TM1 (POTENTIAL).
TM2 (POTENTIAL).
TM4 (POTENTIAL).
TM4 (POTENTIAL).
TM5 (POTENTIAL).
; 6E8EB394 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
D3212F8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AGMLNYRMWQDNQVRRSGRRLSE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
67
100
126
155
18927 AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.5%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52291; G46000; -. EMBL; Z11165; G46125; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                           RECEPTOR; TRANSMEMBRANE.
TRANSMEM 6 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (REL. 15,
01-AUG-1990 (REL. 15,
01-OCT-1994 (REL. 30,
                                                                                                                                                                                                                                                                                                                                       80 1
106 1
135 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRIK_RHOCA
P17057;
                                                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
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TRANSMEM
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ERMINIA CHRYSANTHEMI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCHERICHIA COLI.
PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>`</u>
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SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                       LINDEBERG M., COLLMER A.;
J. BACTERIOL. 174:7385-7397(1992).
-!- FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND METHYLATES
THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97061202.
OSHIMA T., ABBA T., FUJITA K., HAYASHI K., HONJO A.,
OSHIMA T., INDA T., ITOH T., KAJIHARA M., KANAI K., KASHIMOTO K.,
KIMURA S., KITAGAWA M., MAKINO K., MASUDA S., MIKI T., MIKOBUCHI K.,
MORI H., MOTOWURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., SANPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y.,
YANDO M., HORIUCHI T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
CHUNG E., ALLEN E., ARAUJO R., APARICIO A., DAVIS K., DUNCAN M.,
FEDERSPIEL N., HYMAN R., KALMAN S., KOMP. C., KURDI O., LEW H., LIN
NAMATH A., OEFNER P., ROBERTS D., SCHRAMM S., DAVIS R.W.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                             (PROBABLE).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C20; ALSO KNOWN AS LI LEADER PEPTIDASE FAMILY.
EMBL; LO2214; G148444; -.
PIR; C47755; C47755.
                                                                                                                                                                                                                                                                                                                                                                                                                                      220 LGAM-LGWQALPNLVLIASLTGLTATLLWQRIHRLSMQQPLAFGPWLAVSGAM 271
                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                              HYDROLASE; PROTEASE; TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUTAWATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLTJ.
                                                                                                                                                                                                                                                                                                                                                                     Score 105; DB 1; Length 283; Pred. No. 4.81e-02;
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.81e-02;
23; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=K12 / BK9MDG;
LUM D., WALLACE B.J.;
SUBMITTED (JUN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
87D636A4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AA
                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                  196
236 PO
279 PO
31355 MW;
                                                                                                                                                                                                                                                                                                                                                                    9.08;
                                                                                                                                                                                                                                                                                                                                                                               Similarity 26.4%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                       128
153
176
216
259
283 AA;
                             ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                     SEQUENCE FROM N.A.
                                                                                 93054355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                  STRAIN-EC16;
MEDLINE; 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8

GLITJECOLI
AC D1 -FEB-1995
DT 01-FEB-1995
DT 01-NOV-1997
GLUTAMATE/AS
GLUTA
OC BUTEROBACTEF
RN [1]
RP SEQUENCE FRC
STRAIN-K12,
RA LUM D, WALL
RN [2]
RP SEQUENCE FRC
STRAIN-K12,
RN [2]
RP SEQUENCE FRC
STRAIN-K12,
RN [2]
RP SEQUENCE FRC
STRAIN-K12,
RN [3]
RP SEQUENCE FRC
STRAIN-K12,
RN [3]
RP SEQUENCE FRC
STRAIN-K12,
RN [3]
RA SEDERSPIEL
RA RAMATH A,
RA FEDERSPIEL
RA NAMATH A,
RA SUBMITTED (
RN [4]
RA SAMPEI G,
RA MORIN H, M
                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
SEQUENCE
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TRANSMEM
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITIED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUNCAN M., ALLEN E., ARAUJO R., APARICIO A.M., CHUNG E., DAVIS K., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LEW H., LIN D., NAMATH A., OFFNER P., ROBERTS D., SCHRAMM S., DAVIS R.W.; SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR ASPARTATE/GLUTAMATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                         (PROBABLE).
SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYDROCINNAMIC ACID).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                        EMBL, 10991; G624630; -.
EMBL, AE000169; G1786874; -.
EMBL, D80599; G1778572; -.
EMBL, D90705; G165173; -.
ECCGENE; EG12661; G17J; -.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
TRANSPORT; AMINO-AG11 TRANSPORT; TRANSPERSENE; INNER MEMBRANE.
TRANSMEM 33 POTENTIAL.
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FERRANDEZ A., GARCIA J.L., DIAZ E.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: COULD BE A TRANSPORTER FOR 3-PHENTLPROPIONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
-!- CAUTION: REP 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFF.
EMBL, AE000142; G1786549; -.
EMBL; D85613; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.58e-01;
16; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 EMMNLVKNSAIASTIGLVDMAAQAGKLLDYSAHAWESFTAITLAY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NASHIMOTO H., SAITO N.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHPT_ECOLI STANDARD; PRT; 418 AA.
P77589; P77037;
01-NOY-1997 (REL. 35, CREATED)
01-NOY-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE 3-HYDROXXPHENYLPROPIONIC ACID TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
39DD60F3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27502 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 8.6%;
Local Similarity 35.6%;
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                 SUBFAMILY.
                                                                                                                      (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12;
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US-09-047-652A-3.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIGAALAATLGFAGANLAWQTV--FWVGGVVPLIL-V-PLLMRWLPESAVFAGEKQSAPP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDP-DIACYLGLYCEROL.

1 PATHWAY: PHOSPHATIDATE = PYROPHOSPHATE +

1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

EMBL; D50811; G1262332; -...
TRANSFERASE; NUCLEOTIDYLTRANSFERASE; PHOSPHOLIPID BIOSYNTHESIS;
TRANSMEBRANE: INNER MEMBRANE.

TRANSMEBRANE:

12 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE
SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEUDOMONAS AERUGINOSA.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
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SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- CATALYTIC ACTIVITY: CTP + PHOSPHATIDATE = PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 271;
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Pred. No. 5.01e-01;
24; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 34; Indels
                                                                                        SYMPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100; DB 1; 1
Pred. No. 2.11e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 LRALF-APETATATLLEWL-CYFFTLLVVYMLINWLPL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWLAF 146
                                                                                                                                                                                                                                                                                                                                                                      -> V (IN REF. 4
AE3D1B8F CRC32;
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               ECOGENE; EG13293; MHPT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE;
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26; Conservative
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Best Local Similarity 27.6%;
Matches 27; Conservative
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Q59640;
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                                                                    01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
GLUCAN 1,4-ALPHA-MALICHEXAOSIDASE PRECURSOR (EC 3.2.1.98) (G6-AMYLASE)
(MALTOHEXAOSE-PRODUCING AMYLASE) (EXO-MALTOHEXAOHYDROLASE).
BACILLUS SP. (STRAIN 707).
                                                                                                                                                                                                                                                         TSURAMOTO A., KINDRA K., ISHII Y., TAKANO T., YAMANE K.;
BIOCHEM. BIOPHYS. RES. COMMUN. 151:25-31(1988).

-1 CATALYITC ACTIVITY: HYDROLESIS OF 1.4 *ALPHA-D-GLUCOSIDIC LINKAGES
IN AMYLACEOUS POLYSACHARIDES SO AS TO REMOYE SUCCESSIVE
MALTOHEXAGSE RESIDES FROM THE NON-REDUCING CHAIN ENDS.

-1 PATHWAY: DEGRADATION OF STARCH.
-1 SUBCELLULAR LOCATION: EXTRACH.
-1 SIDILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.

PIR; A27705, A27705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i-FUNCTION: CHICARDLAST OMEGA-3 FRITY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BLOSYNTHESIS OF 16:3 AND 18:3 FATTY
ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
TO USE FERREDOYIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERFIED TO GALGACTOLIFIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
-I-PATHWAY: POLYUNSATURATED FATTY ACID BLOSYNTHESIS.
-I-SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (FROBABLE).
-I-DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
AND/ OR BE INVOLUDED IN METAL ION BINDING.
-I-SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
                                                                                                                                                                                        PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
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EUKARYOTA: PLANTA: EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SCROPHULARIALES; PEDALIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALTOHEXAOSE-PRODUCING AMYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97; DB 1; Length 518;
Pred. No. 5.01e-01;
"...matches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 WI-PPAWKGASQNDVGYGAYDLY-DLGEFNQKGTV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 AA
                                   518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: | | | : : : | | : : | | . | . | 47 WVLGPVW-GTLXSAMGYGSYLVWKELGGFTEKAVV 80
                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 34-36
                                     PRT;
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Best Local Similarity 37.1%;
Matches 13; Conservative
                                   STANDARD;
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11
AMT6_BACS7
P19571
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FD3C_SESIN
P48620;
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               RESULT
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B., GOFFEAU A.;

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 SCT1 OR YBL011W OR YBL0315 OR YBL0309
                                                                                                                                                                             MEDLINE; 93070615.
SKALA J., VAN DYCK L., PURNELLE
YEAST 8:777-785(1992).
                                                                                               MATSUSHITA M., NIKAWA J.;
J. BIOCHEM. 117:447-451(1995)
                                                                                   MEDLINE; 95332274.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                SEQUENCE FROM N.A.
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OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHLOROPLAST (POTENTIAL).
OMEGA-3 FATTY ACID DESATURASE,
CHLOROPLAST.
                                                                                                                                                                                                                                                DB 1; Length 447;
                                                                                                                                                                                                                             119 WRSMG-YVVRDVAVVFGLAAVAAYFNNWVVWPLYWFAQSTMFWALFVL 165
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Pred. No. 8.83e-01;
24; Mismatches 26; Indels
                                                                                                                                                                                              8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                              Score 95; DB 1; L
Pred. No. 8.83e-01;
                                                                            171 HISTIDINE BOX 1.
207 HISTIDINE BOX 2.
374 HISTIDINE BOX 3.
51116 MW; 67B2C46B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
D447799A CRC32;
                                                                                                                                                                                                                                                                                                         FUR4_SCHPO STANDARD; PRT; 589 AA. 010279.  
10.007-1997 (REL. 35, CREATED)  
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCT1_YEAST STANDARD; PRT; 759 AA. P32784; Q07062; C1-CT-1993 (REL. 27, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) C1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) CTR1 SUPPRESSOR PROTEIN.
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Best Local Similarity 26.3%;
Matches 21; Conservative
                                                                                                                                                            Match 8.1%;
Local Similarity 33.3%;
les 16; Conservative
                                446
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212
2512
2952
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589
AA;
                                                                                                                              447 AA;
                 FRANSIT PEPTIDE
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA
CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95180446.
WAKIYAMA M., SHIOKAWA K., MIURA K.I.;
FEBS LETT. 360:191-193(1995).
FEBS LETT. 360:191-193(1995).

-1- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE- CONTAINING SYNTHESIS AND FACILITATES RIBOSONE BINDING BY INDUCING THE UNWINDING OF THE MRNAS SECONDARY STROCTURES.

-1- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EIF4A (WHICH CAN CYCLE IN AND OUT OF THE COMPLEX).

FEMBL; D31837; G849076; --
PROSITE; PS00813; IF4E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
               MEDLINE; 93070613.
MEDLINE; 93070613.
MEDLINE; 93070613.
MEDLINE; 93070613.
DELAVENU T., JACQ C., PEREA J.;
YEAST 8:761-768(1991).
-!- FUNCTION: MULTICOPY SUPPRESSOR OF THE CTRI MUTATION.
-!- SIMILARITY: STRONG, TO YEAST YRR067W.
EMBL; 235773; G535999; -.
EMBL; 235773; G535999; -.
EMBL; 23573; G55399; -.
EMBL; S25330; S25330.
TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ښ
ښ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 1; Length 759;
Pred. No. 1.17e+00;
16; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLU.

S -> F (IN REF. 2).

R -> A (IN REF. 2).

A -> P (IN REF. 2).

A -> P (IN REF. 2).

S -> G (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 YQVSPLAARLLYPYLAWLAFTTTLNYCVWRDNHGWRGGRRLPE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 YOEPSATKKILYSIATWLLYNI-FH-CFFREIRG-RGSFKVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 AA
                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85723 MW;
SEQUENCE OF 609-759 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.0%;
Best Local Similarity 27.9%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
730
759 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 15
IF4E_XENLA
P48597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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INITIATION FACTOR; PROTEIN BIOSYNTHESIS; RNA-BINDING. SEQUENCE 213 AA; 24635 MW; 4F60C133 CRC32;
  S S
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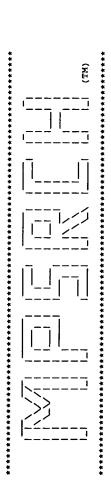
		ŷ
		Gaps
		6;
jth 213;		Indels
Lenc	; 0	47;
Ouery Match 7.9%; Score 92; DB 1; Length 213;	. 2.03e+C	natches
e 92	. N	Mis
Scor	Pred	18;
7.98;	25.3%;	vative
	ilarity	Conser
4	Sim	24;
Matc	Local	89
Query	Best	Match

8 S

g S

Search completed: Tue Jul 21 14:54:26 1998 Job time : 18 secs.

CONTRACTOR OF THE PARTY OF THE



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Jul 21 14:54:44 1998; MasPar time 12.32 Seconds 577.651 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-047-652A-3 (1-169) from USO9047652A.pep 1170 1 XXXXXXXXXXXXXXXXXXXXXXIII Title: Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

140542 segs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1.sp_fung1 2.sp_human 3.sp_invertebrate 4.sp_mammal
5.sp_mhc 6.sp_organelle 7.sp_phage 8.sp_plant
9.sp_bacteria 10.sp_rodent 11.sp_virus 12.sp_vertebrate
13.sp_unclassified

Mean 42.037; Variance 94.668; scale 0.444 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Gaps ö

Length 169;

Query Match 85.0%; Score 995; DB 10; Length 16 Best Local Similarity 83.2%; Pred. No. 4.27e-156; Matches 119; Conservative 14; Mismatches 10; Indels

147 ATVLNYYWRDNSGRRGGSRLAE 169 :| || || || || || || || || 111 147 TTTLNYCVWRDNHGWRGGRRLPE 169

01, CREATED) 01, LAST SEQUENCE UPDATE) 01, LAST ANNOTATION UPDATE)

169 AA.

PRT;

PRELIMINARY;

ULT 2 013850 013850; PRELIMINAR: 013850; 013850; 01-NOV-1996 (TREMBLREL. 0: 01-NOV-1996 (TREMBLREL. 0:

RESULT ID 011 AC 011 DT 011 DT 01

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ID Description
262118 BENZODIAZEPINE RECEPTO
213850 PERIPHERAL BENZODIAZEP
D28797 MITOCHONDRIAL BENZODIA
254791 CRT GENES.
293367 HYPOTHETICAL PROTEIN C
260419 MITOCHONDRIAL BENZODIA
034694 YTAB PROTEIN.
P74502 HYPOTHETICAL
Q55465 HYPOTHETICAL
045384 PUTATIVE GTG
P73514 HYPOTHETICAL
034416 YOAV.
230838 MHC CLASS I PROTEIN PR
D23802 PLASTID OMEGA-3 FATTY
240118 DELTA-15 LINEOYL DESAT
P71879 HYPOTHETICAL
006630 HYPOTHETICAL
005804 HYPOTHETICAL 40.5 KD
004807 OMEGA-3 FATTY ACID DES
239553 RNA POLYMERASE

WUB GE 1 9 KD P 2 URASE 2 URASE. 2 1 D DES 3 1 KD P 3 ROME 0 4	20 A 200 H H H H H H H H H H H H H H H H H H	IENTS  '; 169 AA.  ED)  SEQUENCE UPDATE)  ANNOTATION UPDATE)  ALL (PERIPHERAL-TYPE BENZODIAZEPINE	A; TETRAPODA; MAMMALIA; MA T., TOKUNAGA R.; CRC32;
8.2 261 9 8.2 354 3 8.1 321 9 8.1 448 8 8.1 448 8 8.0 637 9 7.9 535 9	92 7.9 676 2 015296 93 7.9 685 8 P993156 91 7.8 117 9 032937 91 7.8 458 6 024406 91 7.8 458 6 024406 90 7.7 332 9 P75413 90 7.7 432 9 P7540 90 7.7 439 11 Q67875 90 7.7 439 1 Q67875 90 7.7 439 1 Q67875 90 7.7 439 1 Q67855 89 7.6 460 9 P77429 89 7.6 461 3 P91197 88 7.5 281 11 Q4774	ALIGNM  1 8; 87 70-1996 (TREMBLREL. 01, CREAT 70-1996 (TREMBLREL. 05, LAST 701AZEPINE RECEPTOR, PERIPHER	MUSENIUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETR EUTHERIA; RODENTIA. EUTHERIA; RODENTIA. SEQUENCE FROM N.A. STRAIN-BALB/C; TAKETANI S., KOHNO H., OKUDA M., FURUKAWA T., TAKETANI S., KOHNO H., OKUDA M., FURUKAWA T., EMBL; D21207; G484054; MGD; MGI:88222; BZRP. SEQUENCE 169 AA; 18829 MW; 90CAC703 CRC32;
2222222 1222222 1222222 122222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1222 1222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 1		RESULT AC 0621: AC 0621: DT 01-N DT 01-N DT 01-N DT 01-N DT 01-N DT 01-N	

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Matches
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KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E.,
KIENK H.P., CLAYTON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., OUACKENBUSH J., LEE N.H., SUTTON G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
KIRKNESS E.F., GOCKER J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
OVERBEEK R., GOCAVIE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

KELENK H.P., CLATYON R.A., TOMB J., WHITE O., NELSON.K.E.,
KETGHOM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., OUGACKENBISH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., WACKENNEY K., ADAMS M.D., LOFFUS B.,
PETERSON S., REICH C.I., WORBIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
COTTON M.D., SPRIGGS T., ARTIAGH P., KAINE B.P., SYRES S.M.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 WAAGPELGMA-PHLL-GARQMGWALVDLLLVSGAAAATTVAWYQVSPLAARLLYPYLAWL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVGSPGPLH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
MITOCHONDRIAL BENZODIAZEPINE RECEPTOR/SENSORY TRANSDUCTION PROTEIN.
AF1475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARCHAEOGLOBUS FULGIDUS.
ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 956; DB 2; Length 169
Pred. No. 7.01e-149;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENTER J.C.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE001001; G2649094; -.
SEQUENCE 153 AA: 17185 MW; F7796417 CRC32;
                                                                                                                                                                                    TISSUE-PLACENTA;
MEDLINE; 94140364.
LIN D., CHANG Y.J., STRAUSS J.F., MILLER W.L.;
GENOMICS 18:643-650(1993).
EMBL; L21954; G488425; -..
EMBL; L21955; G488425; JOINED.
EMBL; L21953; G488425; JOINED.
SEQUENCE 169 AA; 18483 MM; E528DC71 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AFTTLNYCVWRDNHGWRGGRRLPE 169
PERIPHERAL BENZODIAZEPINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AFATTLNYCVWRDNHGWHGGRRLPE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 81.7%;
Local Similarity 86.2%;
les 125; Conservative
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
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SOSSERVEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ILWIPVFFGMKRMATALAVVWVMWLFVAATMWAFFQLDTWAGVLFVPYLIWATAATGLNF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 WYAGLOKPSWHPPHWYLGPVWGTLYSAMGYGSYLVWKELGGFTEKAVVPLGLYTGQLALN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 WYDNLNKPWWNPPRWVFPLAWTSLYFLMSLAPC-GWR--SS-KVRAGAGL-LCA-QLAFN 83
                                                                                                                                                                                                          31 WYAGVEKPFFTPPNWLFGPAWTLLYFLIGIVLYIAW-E-NGFWNDSRVKATFFT-QLGLN 87
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
COULSON A., CRAXYON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
FULTON L., GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER R.,
LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHODOBACTER SPHAEROIDES (RHODOPSEUDOMONAS SPHAEROIDES).
PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
                                                                                                     ..
ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
9
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Length 153;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CRT GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TREMBLREL. 02, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN C41G7.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LANG H.P., COGDELL R.J., TAKAICHI S., HUNTER C.N.; J. BACTERIOL. 177:2064-2073(1995).
EMBL, 824589; 675409; -. SEQUENCE 157 AA; 17854 MW; D56D5781 CRC32;
Score 327; DB 9;
Pred. No. 8.96e-36;
                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
27.9%;
39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAENORHABDITIS ELEGANS
                                     Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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MEDLINE; 95238278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHODOSPIRILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 FAI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 YCV 154
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
1D 054791
DT 01-NOV-
DT 01-NOV-
DE CRT GEN
GN CRTK.
GN RHODOSP
CC RH
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STRAIN-PCC6803;
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P74502
P74502;
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PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                               421 WWAALKKPNWAPKDVRVYSAV-DLLTLSPLGYASYLVYKNGGGFDYNDTKLALGLYGASV 479
                                                                                                                                                                                       480 TLAVATIPIV-KKKELGCLWKNTTVVSLTAAAASFAFYKIDKKAGLLVVPFAVWTAFYAY 538
                                                                                                                                                                                                   KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
                                                                                                                             5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                  CRICETULUS GRISEUS (CHINESE HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E. STADEN R., SHOSTON J., THIERY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSON S., WATESON R., WATESON R., WATESON R., WATESON B., WATURE 368:32-38(1994).

EMBL: Z81048; E348255; --
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                    Score 245; DB 3; Length 553;
Pred. No. 3.72e-22;
32; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 211; DB 10; Length 31 Pred. No. 9.88e-17; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                060419 PRELIMINARY; PRT; 31 AA.
060419 0100401996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
MITOCHONDRIAL BENZODIAZEPINE RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 95237610.
YAROVLEV A.G., FUFFO M., JURKA J., KRUEGER K.E.;
GENE 155:201-205(1995).
EMBL: U12420; G529944; -.
                                                                                   553 AA; 61142 MW; A2548F6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 AA; 3275 MW; 3D86A9D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 WPPIFFGARQMGWALVDLLLVSGAAAATTVA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WPPIFFGARQMGWALADLLLVSGVATATTLA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05,
05,
                                                                                                     Query Match
Best Local Similarity 35.7%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.0%;
Local Similarity 87.1%;
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       034694,
034694;
01-JAN-1998 (TREMBLREL: 0
01-JAN-1998 (TREMBLREL: 0
01-JAN-1998 (TREMBLREL: 0
                                                                                                                                                                                                                                539 LAYSIKKEN 547
                                                                                                                                                                                                                                            150 LNYCVWRDN 158
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NON_TER
SEQUENCE
                                                                                    SEQUENCE
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BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
A CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
DENIZOT F., DEVINE K.M., DUSTERHOFT A., ERRALICH S.D., EMMERSON P.T.,
A DENIZOT F. C., TOLITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
A GUISEPLI G., GLASEP P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HOLLO M.F., ITAYA M., JONES L.,
JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
A COBATASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
A KURITA K., LAPIDUS A., LAKDINOIS S., LAUBER J., LAZAREVIC V.,
A KURITA K., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
A MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NARAI S., NOBACK M.,
NOONE D., O'REILLY M., OGRAM R., OGIWARA A., SERSONT A., SARESEAN E., PURNELLE D., PORNOLLIK S., PRESCOTT A.,
A RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
SATO T., SCANLAN E., SCHLEICH S., SCHROFTER R., SCOFFONE F.,
SEKIGCHI J., SEROWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDO
SEKIGCHI J., SEKOWSKA A., TAKAGI T., TAKAHARA P., TAKAMARA T.,
ANBUTTER P., WAMBUTH R., WEDLER E., WEDLER F., VASSAROTTI A.,
VINAIT A., WAMBUTH R., WEDLER E., WEDLER H., WHITESPER P., WINTER P., WINTERS P., WINTER P., WINTERS P., WINTER P., YAMMOTO R., YAMANE K., YOSHIKAWA H.F., DANCHIN A.,
ANDURE S., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
ANTURE 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 WYNSLKKPDWTPSGTAIGIIWAILFALISLSAAIVYAAFS-FKGAKSFWFTLLIN-YVLN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 160; DB 9; Length 155;
Pred. No. 5.49e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNECHCUXSILS SF.
EUBACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z99119; E1185966; -.
EMBL; AF008220; G2293285; -.
SEQUENCE 155 AA; 17288 MW; 875DAD85 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
HYPOTHETICAL 17 8 KD PROTEIN.
SYNECHOCYSTIS SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIEL J.A., BOELS J.M., BELDMAN G., VENEMA MOL. MICROBIOL. 11:203-218(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity 27.9%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 LRWFNRLRRPSWLTFEWAIPFIWIAIFIAGAISATLAWNATADPGHRWGLMVGYLLLELT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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PROKARYOTA; BACTERIA; GRACILICUTES; OXYPHOTOBACTERIA; CYANOBACTERIA;
CHROOCOCCALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KANEKO T., TANKKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIDRA M., TABATA S.; SUGIDRA M., TABATA S.; DNA RES. 2:153-166(1995).
EMBL: D64006; G1001322; ---
HYPOTHETICAL PROTEIN.
SEQUENCE 634 AA; 69363 MW; BCEC37CB CRC32;
                                                                                                                                                                             BONDETELLA PERTUSSIS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.0%; Score 105; DB 9; Length 634;
Best Local Similarity 30.0%; Pred. No. 1.55e-01;
Matches 15; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 130; DB 9; Length 159
Pred. No. 9.21e-05;
30; Mismatches 55; Indels
TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 9
055465
055465
055465
0.05465.
01.NOV-1996 (TREMBLREL. 01, CREATED)
01.NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01.NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
HYPOTHETICAL 69.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AA; 17809 MW; 9EA93412 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, BPUTATIVE GTG START CODON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1)
SEQUENCE FROM N.A.
STRAIN-PCC6803;
MEDLINE; 96127529.
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BP536;
                                                                                                                                                         STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 10
Q45384
Q45384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
1D Q4
AC Q44
DT 011
DT 011
DT 011
DD 02
DD PE PU
DD PR BP
OC PR
OC PR
OC PR
CO PR
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Pred. No. 3.58e-01;
24; Mismatches 23; Indels 12; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AWVSPCQWG-TTLWLGAVFLAAG-G--LVLGKVGRW-DTSIMFLAVYAGLDLARNAWLGW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
                                                                                                                               Length 188;
                                                                                                                      Score 102; DB 9; Length 188
Pred. No. 3.58e-01;
10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNECHOCYSTIS SP.
EUBACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
ALLEN A.G., MASKELL D.J.;
MOL. MICROBIOL. 19:37-52(1996).
EMBL; X90711; G992979; -.
SEQUENCE 188 AA; 21467 MW; F6C7644C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 AA
                                                                                                                                                                                                        121 TGGVWYNINDMATALVFANLIWLLIKRKLSF 151
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 PPEVSFHHLENGSLLVFALFMLTDP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || : | : | || |:::: :
|PP-IFFGARQMGWALV-DLLLVSGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL 32.0 KD PROTEIN.
                                                                                                                      %.7%;
Local Similarity 29.0%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 8.7%;
Local Similarity 30.6%;
les 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05,
05,
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01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JLT 12
034416
034416;
                                                                                                                                            Best Loca
Matches
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Matches
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11D 03
AC 03
DT 03
DT 01
DT 0
    SARA
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Wed Jul 22 12:34:50 1998
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AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
BARDOLLLES S., RRUGSHI C.V., CALDWELL B., CAPUANO V., CARFER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
A BYTIAN K.D., ERRINGTON J., FARRET C., FERRARI E., FOULGER D.,
A GILSEPPI G., GUSTER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
A GILSEPPI G., GUSTER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAXA M., JONES L.,
A HILBERT H., KOETTER P., KONINGSTEIN G., KROCH S., KUMANO M.,
A KURITA K., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
A KURITA K., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
A KURITA K., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
A HESE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
A HODONE D., O'REILLY M., OGAWA K., OUDEGA B., PARK S.H.,
A RAND C., POHL T.M., PORTETELLE D., PORMOLLIK S., PRESECAT A.M.,
A RAND C., POHL T.M., PORTETELLE D., PORMOLLIK S., REY M., REYNOLDS S.,
A STROGULI J., SEKOWSKA A., SEROR S.J., SEROR P., SHIN B.S., SOLDO B.,
A SKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., YANGANE Y., VANDENBOL M., VANNIER F., VASSAROTTI A.,
A TAKAUCHI M., TAMAKOSHI A., TAKAMARA T., TAKEMARA T., TAKAMARA T., YANGANE F., VASSAROTI A.,
A TAKAUCHI M., TAMAKOSHI A., TAKAMARA T., YANGANE F., VASSAROTI A.,
A TAMA TAKEUCHI M., TAMAKOSHI A., TAKAMARA T., YANGANE F., VASSAROTI A.,
A TAKAUCHI M., TAMAKOSHI A., TAKAMARA T., YANGANE F., VASSAROTI A.,
A TAKAUCHI M., TAMAKOSHI A., TAKAMARA T., TAKAMARA T., YANGANE F., VANDENBOL M., VANNIER F., VASSAROTI A.,
A TAKAUCHI M., TAMAKOSHI A., TAKAMARA T., YANGANE K., YANGANE K., YANGANE K., YOSHIKAWA H.F., YANGANE K.,
A YOSHIDA K., YOSHIKAWA H.F., YANGANE K., YOSHIKAWA H.F., YANGANE K.,
ANGANE D., OKANIKA H.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 SAEWIYQAVWSLLFNGLLSTGFIFVVWFWVLNQIQASKASMAL-MFVPVLALFFGW 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 PPHWVLGPVWGTLYSAM-GYG-SYLVW-KELGGF-TEKAVVPLGLYTGQLALNWAW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
MHC CLASS I PROTEIN PRECURSOR.
OVIS ARIES (SHEEP).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHBRIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DOBJ DATA BANKS.
EMBL; AF027868; G2619001;
EMBL; 299114; E1185349;

        SIGNAL
        1
        28
        POTENTIAL.

        CHAIN
        29
        368
        POTENTIAL.

        SEQUENCE
        368
        AA, 41442
        MW, 9825CEDA CRC32;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AA; 33044 MW; 2CD69019 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT; 368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 90375196.
GROSSBERGER D., HEIN W.R., MARCUZ A.;
IMMUNOCENETICS 32.77-87(1990).
EMBL; M34676; G166002; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CT 13
Q30838
Q30838;
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STRAIN-CV. CHIHOKU; TISSUE-LEAF;
HORIGUCHI G., IWAKAWA H., KODAMA H., KAWAKAMI N., NISHIMURA M., IBA K.;
PHYSIOL. PLANTRRUM 96:275-283(1996).
EMBL; D43688; D1008371; -.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 WSSMG-YVVRDVVVVLALAATAARLDSWLAWP-VYWAAQGTMFWALFVLGHDCGHGSFSN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DELTA-15 LINEOYL DESATURASE.
LIMNANTHES DOUGLASII.
EUKARYOTA; PLANTAE; EMBRYOBIONTA; MAGNOLIOPHYTA; MAGNOLIOPSIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA: PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
CYPERALES; GRAMINEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99; DB 8; Length 436;
Pred. No. 8.16e-01;
11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; DB 8; Lt
Pred. No. 8.16e-01;
17; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBLIA R. S., MACKENZIE S.L.;
PLANT PHYSIOL. 108:861-861(1995).
EMBL; U17063; G699390; -.
SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 AA.
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                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQ
01-JAN-1998 (TREMBLREL. 05, LAST ANN
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROSIDAE; GERANIALES; LIMNANTHACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 NAKLNSVVGHILHSSILVPYNGW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 TVAWYOV-SP-LAARLLYPYLAW 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.9%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.5%;
Best Local Similarity 36.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                        TAFAD7.
TRITICUM AESTIVUM (WHEAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 95334518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Job time : 52 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CT 15
040118
040118;
                                                                                                                              CT 14
023802
023802;
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Query Match
8.5%; Score 100; DB 5; Length 368;
Best Local Similarity 40.0%; Pred. No. 6.21e-01;
Matches 18; Conservative 5; Mismatches 19; Indels

293 GL-QEPLTLRWEPPQTSFLTSSMG-IIVGLVLLVMVAVVAAAVIW 335

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